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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

(57) Abstract

Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.

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COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD

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The present invention relates generally to the detection and therapy of breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. *See*, *e.g.*, Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in

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breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated DNA molecules are provided, comprising (a) a nucleotide sequence preferentially expressed in breast cancer tissue, relative to normal tissue; (b) a variant of such a sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% (preferably no more than 5%) of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one of the above sequences. In one embodiment, the isolated DNA molecule comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated DNA molecule comprises a nucleotide sequence recited in any one of SEQ ID NO: 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

In related embodiments, the isolated DNA molecule encodes an epitope of a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219,

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221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297; and wherein RNA corresponding to said nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In another embodiment, the present invention provides an isolated DNA molecule encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a DNA molecule as described above are also provided.

In related aspects, the present invention provides recombinant expression vectors comprising a DNA molecule as described above and host cells transformed or transfected with such expression vectors.

In further aspects, polypeptides, comprising an amino acid sequence encoded by a DNA molecule as described above, and monoclonal antibodies that bind to such polypeptides are provided.

In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208,

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215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

Within a related aspect, the diagnostic kit comprises a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for an RNA molecule described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of an RNA molecule as described above, or an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a DNA molecule described herein. In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a DNA molecule as described above, or a DNA molecule selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In another

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embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA molecule encoding a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected form the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, -217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immune response enhancer or adjuvant, are provided. In yet other aspects, the present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2)

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and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

Figure 4 is a genomic clone map showing the location of additional -retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

Figure 9 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

Figure 14 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG1.

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Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA has a sequence.

Figure 21Al depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

Figure: 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer.

The compositions described herein include polypeptides, nucleic acid sequences and antibodies. Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (i.e., the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-

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specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Nucleic acid sequences of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retreviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141). Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 -SEQ ID NO:10. B18Ag1 has homology to the gag p30 gene of the endogenous human retroviral element S71, as described in Werner et al., Virology 174:225-238 (1990) and also shows homology to about thirty other retroviral gag genes. As discussed in more detail below, the present invention also includes a number of additional breast tumorspecific polypeptides, such as those encoded by the nucleotide sequences recited in SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins containing the sequences recited herein. A polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may (but, need not) possess immunogenic or antigenic properties.

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An "epitope," as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

The compositions and methods of the present invention also encompass variants of the above polypeptides and nucleic acid sequences encoding such polypeptides. A polypeptide "variant," as used herein, is a polypeptide that differs from the native polypeptide in substitutions and/or modifications, such that the antigenic and/or immunogenic properties of the polypeptide are retained. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antisera and/or T-cells as described above. Nucleic acid variants may contain one or more substitutions, deletions, insertions and/or modifications such that the antigenic and/or immunogenic properties of the encoded polypeptide are retained. One preferred variant of the polypeptides described herein is a variant that contains nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions.

Preferably, a variant contains conservative substitutions. A 30 "conservative substitution" is one in which an amino acid is substituted for another

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amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenic or antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

In general, nucleotide sequences encoding all or a portion of the polypeptides described herein may be prepared using any of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential display PCR. This technique compares the amplified products from RNA template prepared from normal and breast tumor tissue. cDNA may be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and subcloned into a suitable vector (e.g., the T-vector, Novagen, Madison, WI). Nucleotide sequences encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID NO::87-125.

Alternatively, a gene encoding a polypeptide as described herein (or a portion thereof) may be amplified from human genomic DNA, or from breast tumor

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cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). An amplified portion of B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11 - SEQ ID NO:86 and SEQ ID NO:142 - SEQ ID NO:297.

Recombinant polypeptides encoded by the DNA sequences described above may be readily prepared from the DNA sequences. For example, supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been

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transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, J. Am. Chem. Soc. 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division,, Foster City, CA, and may be operated according to the manufacturer's instructions.

In specific embodiments, polypeptides of the present invention encompass amino acid sequences encoded by a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297, variants of such polypeptides that are encoded by DNA molecules containing one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, and epitopes of the above polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240,

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243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. DNA molecules according to the present invention include molecules that encode any of the above polypeptides.

In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, Eur. J. Immunol. 6:511-519 (1976), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as

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described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis, transferred to a suitable membrane and allowed to react with the antibody. The

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presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane.

Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of

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antibody ranging from about 10 ng to about 1 µg, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, - c.g., Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20^{TM} (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least, 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium

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may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20[™]. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor tissue. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients, without breast cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value may be considered positive for breast

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cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., Clinical Epidemiology: A Basic Science for Clinical Medicine, p. 106-7 (Little Brown and Co., 1985). Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that, would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the

membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μg . Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (e.g., a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an evaluation may be achieved using any of a variety of methods known to -those of ordinary skill in the art such as, for example, in situ hybridization and amplification by polymerase chain reaction.

For example; polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above biological samples. Sequence-specific primers for use in such amplification may be designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86 and 142-297, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one 15 suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art. Amplification is typically performed on samples obtained from matched pairs of tissue 20 (tumor and non-tumor tissue from the same individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a DNA/RNA molecule" means an oligonucleotide sequence that has at least about 80% identity preferably at least about 90% and more preferably at least about 95%, identity to the 30 DNA/RNA molecule in question. Primers and/or probes which may be usefully

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employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers comprise at least about 10 contiguous nucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide staining while important in defining gene specificity do not lend themselves to diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can be modified for use in 96 well plate formats. Instrumentation to perform such methodologies are available from Perkin Elmet/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxygenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

In yet another method for determining the presence or absence of breast cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to a test antigen (i.e., an immunogenic

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portion of a polypeptide employed, or a variant thereof). The response may measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 µg to 100 µg, preferably from about 10 µg to 50 µg in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80^{TM} .

In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast, breast cancer is not progressing when the signal detected either remains constant or decreases with time.

In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the compounds (which may be polypeptides, antibodies or nucleic acid molecules) are preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more polypeptides and an immune response enhancer, such as an adjuvant or a liposome (into which the compound is incorporated) Pharmaceutical compositions and vaccines may additionally contain a delivery system, such as biodegradable microspheres which are disclosed, for example, in U.S. Patent

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Nos. 4,897,268 and 5,075,109. Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, including one or more separate polypeptides.

Alternatively, a vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated in situ. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the - necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). 10 Bacterial delivery systems involve the administration of a bacterium (such as Bacillus-Calmette-Guerrin) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., Science 259:1745-1749 (1993), and reviewed by Cohen, Science 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as, carriers for the pharmaceutical compositions of this invention.

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Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. To prevent the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a patient with breast cancer, the pharmaceutical composition or vaccine may comprise one or more polypeptides, antibodies or nucleotide sequences complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients.

A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*.

5 Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more -polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

The following Examples are offered by way of illustration and not by way of limitation.

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EXAMPLES

EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC CDNAs USING DIFFERENTIAL DISPLAY RT-PCR

This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO.:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (CTTCAACCTC) (SEQ ID NO.:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products was obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus, (SSV). S71 contains an incomplete gag gene, a portion of the pol gene and an LTR-like structure at the 3' terminus (see Werner et al., Virology 174:225-238 (1990)). B18Ag1

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is also 64% identical to SSV in the region corresponding to the P30 (gag) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of gag proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the gag gene, but spans several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C \rightarrow 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence -present at relatively high levels in the patient's breast tumor tissue. The primers used in amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO.:128) and B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO..129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ JD NO.:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127) at 2 mM magnesium at pH 9.5. The same experiments showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (see Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the B18Ag1 transcript is not present in various normal tissues (including lymph node, myocardium and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent, prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin,

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lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be present in human genomic DNA as a single copy endogenous retroviral element. A genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion. Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 11-22.

Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic 25 clone. The box below this line shows the position of selected restriction sites. The arrows depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within the element. The open boxes correspond to predicted reading frames, starting with a

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methionine, found throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%) compared to the genomic sequence shown in SEQ ID NO:141.

B. <u>Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides</u>

Normal RNA and tumor RNA was prepared and mRNA was isolated and converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above. Differential display PCR was then executed using the randomly chosen primers SEQ ID NO.: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcioned into either the T-vector (Novagen, Madison, WI) or the pCRII vector (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO:11-26 and 28-77) (see also Figures 6-20).

An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene bank as described above, revealed homology to the known human β -A activin gene.

Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In further studies, six different splice forms of the antigen B11Ag1 were isolated, with each of the various splice forms containing slightly different versions of

the B11Ag1 coding frame. Splice junction sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the original B11Ag1 clone, with expression being breast tumor, prostate and testis-specific. The determined cDNA sequences for the isolated protein coding exons are provided in SEQ ID NO: 292-297, respectively.

EXAMPLE 2

PREPARATION OF B18AG1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA using 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

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EXAMPLE 3

PREPARATION OF B18AG1 DNA FROM BREAST TUMOR CDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μl. After first strand synthesis, the cDNA is diluted approximately 25 fold and 1 μl is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18AG1

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This Example illustrates the identification of B18Ag1 epitopes.

The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for hydrophobicity and hydrophobicity values using the method of Hopp, *Prog. Clin. Biol. Res.* 172B:367-77 (1985) or, alternatively, Cease et al., *J. Exp. Med.* 164:1779-84 (1986) or Spouge et al., *J. Immunol.* 138:204-12 (1987). Additional Class II MHC (antibody or B-cell) epitopes can be predicted using programs such as AMPHI (e.g., Margalit et al., *J. Immunol.* 138:2213 (1987)) or the methods of Rothbard and Taylor (e.g., EMBO J. 7:93 (1988)).

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems Division, Foster City, CA) and techniques such as Merrifield synthesis. Following, synthesis, the peptides can used to screen sera harvested from either normal or breast cancer patients to determine whether patients with breast cancer possess antibodies

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reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can also be tested for their ability to generate a serologic or humoral immune in animals (mice, rats, rabbits, chimps etc.) following immunization in vivo. Generation of a peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC molecules. (see, e.g., Rammensee et al., Immunogeneues 41:178-228 (1995)). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (e.g., Sette et al., J. Immunol. 153:5586-92 (1994)) and more importantly can be tested for their ability to generate antigen reactive cytotoxic Tcells following in vitro stimulation of patient or normal peripheral mononuclear cells using, for example, the methods of Bakker et al., Cancer Res. 55:5330-34 (1995); Visseren et al., J. Immunol. 154:3991-98 (1995); Kawakami et al., J. Immunol. 154:3961-68 (1995); and Kast et al., J. Immunol. 152:3904-12 (1994). Successful in vitro generation of T-cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following in vitro peptide stimulation further confirms the immunogenicity of the B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following in vivo immunization in mice rendered transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., J. Exp. Med. 173:1007-15 (1991).

A representative list of predicted B18Ag1 B-cell and T-cell epitopes, broken down according to predicted HLA Class I MHC binding antigen, is shown below:

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI

QGAAQKPINLSKXIEVVQGHDE

SPGVFLEHLQEAYRIYTPFDLSA

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

YLLVGIQGA

5 GAAQKPINL

NLSKXIEVV

EVVQGHDES

HLQEAYRIY

NLAFVAQAA

10 FVAQAAPDS

EXAMPLE 5

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY DIFFERENTIAL DISPLAY PCR

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The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

To ensure the semiquantitative nature of the RT-PCR, β-actin was used as internal control for each of the tissues examined. Serial dilutions of the first strand cDNAs were prepared and RT-PCR assays performed using β-actin specific primers. A dilution was then selected that enabled the linear range amplification of β-actin template, and which was sensitive enough to reflect the difference in the initial copy, number. Using this condition, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase

treatment and by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

Familia F		
Equally Expressed in Normals and Tumor		16%
Over-expressed in Breast Tumors but	× ' ::,	9%
		970
Expressed in Some Normal Tissues		30%
Over-expressed in Breast Tumors but		61%
	Over-expressed in Breast Tumors but Expressed in Some Normal Tissues Over-expressed in Breast Tumors but	Over-expressed in Breast Tumors but not in any Normal Tissues Over-expressed in Breast Tumors but Expressed in Some Normal Tissues Over-expressed in Breast Tumors but

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
- (iii) NUMBER OF SEQUENCES: 297
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 04-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.419C2
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTA Leu 1	GAG Glu	ACC Thr	CAA Gln	TTG Leu 5	GGA Gly	CCT Pro	AAT Asn	TGG Trp	GAC Asp 10	CCA Pro	AAT Asn	TTC Phe	TCA Ser	AGT Ser 15	GGA Gly	48
GGG Gly	AGA Arg	ACT Thr	TTT Phe 20	GAC Asp	CAT Asp	TTC Phe	CAC His	CGG Arg 25	TAT Tyr	CTC Leu	CTC Leu	GTG Val	GGT Gly 30	ATT Ile	CAG Gln	96
GGA Gly	GCT Ala	GCC Ala 35	CAG Gln	AAA Lys	CCT Pro	ATA Ile	AAC Asn 40	TTG Leu	TCT Ser	AAG Lys	GCG Ala	ATT Ile 45	GAA Glu	GTC Val	GTC Val	144
CAG Gin	GGG Gły 50	CAT His	GAT Asp	GAG Glu	TCA Ser	CCA Pro 55	GGA Gly	GTG Val	TTT Phe	TTA Leu	GAG Glu 60	CAC His	CTC Leu	CAG Gln	GAG Glu	192
												CCC Pro				240
CAT	GCT Ala	CTT Leu	AAT Asn	TTG Leu 85	GCA Ala	TTT Phe	GTG Val	GCT Ala	CAG Gln 90	GCA Ala	GCC Ala	CCA Pro	GAT Asp	AGT Ser 95	AAA Lys	288
AGG Arg	AAA Lys	CTC Leu	CAA Gln 100	AAA Lys	CTA Leu	GAG Glu	GGA Gly	TTT Phe 105	TGC Cys	TGG Trp	AAT Asn	GAA Glu	TAC Tyr 110	CAG Gln	TCA Ser	336
				AGC Ser												363

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

65 70 75 80

His Ala Leu Asn Leu Ala Phe Val Ala Gin Ala Ala Pro Asp Ser Lys
85 90 95

Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser
100 105 110

Ala Phe Arg Asp Ser Leu Lys Gly Phe
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.3:

TCTTAGAATC TTCATACCCC GAACTCTTGG GAAAACTTTA ATCAGTCACC TACAGTCTAC 60 CACCCATTTA GGAGGAGCAA AGCTACCTCA GCTCCTCCGG AGCCGTTTTA AGATCCCCCA TCTTCAAAGC CTAACAGATC AAGCAGCTCT CCGGTGCACA ACCTGCGCCC AGGTAAATGC 180 CAAAAAAGGT CCTAAACCCA GCCCAGGCCA CCGTCTCCAA GAAAACTCAC CAGGAGAAAA 240 GTGGGAAATT GACTTTACAG AAGTAAAACC ACACCGGGCT GGGTACAAAT ACCTTCTAGT 300 ACTGGTAGAC ACCTTCTCTG GATGGACTGA AGCATTTGCT ACCAAAAACG AAACTGTCAA 360 TATGGTAGTT AAGTTTTTAC TCAATGAAAT CATCCCTCGA CGTGGGCTGC CTGTTGCCAT 420 AGGGTCTGAT AATGGAACGG CCTTCGCCTT GTCTATAGTT TAATCAGTCA GTAAGGCGTT 480 AAACATTCAA TGGAAGCTCC ATTGTGCCTA TCGACCCAGA GCTCTGGGCA AGTAGAACGC 540 ATGAACTGCA CCCTAAAAAA ACACTCTTAC AAAATTAATC TTAAAAAACCG GTGTTAATTG 600 TGTTAGTCTC CTTCCCTTAG CCCTACTTAG AGTTAAGGTG CACCCCTTAC TGGGCTGGGT 660 TCTTTACCTT TTGAAATCAT NTTTNGGAAG GGGCTGCCTA TCTTTNCTTA ACTAAAAAAN 720 GCCCATITGG CAAAAATTTC NCAACTAATT TNTATGTNCC TACGTCTCCC CAACAGGTAN 780 AAAAATCING IGGCCTTTIC AAGGAACCAI CCCAICCAIT CCINAACAAA AGGCCIGCCN 840 TTCTTCCCCC AGTTAACTNT TTTTTNT'AA AAT1CCCAAA AAANGAACCN CCTGCTGGAA AAACNCCCCC CTCCAANCCC CGGCCNAAGN GGAAGGTTCC CTTGAATCCC NCCCCCNCNA 960 ANGGCCCGGA ACCNITAAAN TNGTTCCNGG GGGTNNGGCC TAAAAGNCCN ATTIGGTAAA 1020 1080 TNTAGNANCN TATTICCCNC C 1101

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1087 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID'NO:4:

TCTAGAGCTG	CGCCTGGATC	CCGCCACAGT	GAGGAGACCT	GAAGACCAGA	GAAAACACAG	60
CAAGTAGGCC	CTTTAAACTA	CTCACCTGTG	TTGTCTTCTA	ATTTATTCTG	TTTTATTTTG	120
TTTCCATCAT	TTTAAGGGGT	TAAAATCATC	TTGTTCAGAC	CTCAGCATAT	AAAATGACCC	180
ATCTGTAGAC	CTCAGGCTCC	AACCATACCC	CAAGAGTTGT	CTGGTTTTGT	TTAAATTACT	240
GCCAGGTTTC	AGCTGCAGAT	ATCCCTGGAA	GGAATATTCC	AGATTCCCTG	AGTAGTTTCC	300

ACGTTAAAAT	CCTATAGGCT	TCTTCTGTTT	TGAGGAAGAG	TTCCTGTCAG	AGAAAAACAT	360
GATTTTGGAT	TTTTAACTTT	AATGCTTGTG	AAACGCTATA	AAAAAAATTT	TCTACCCCTA	420
GCTTTAAAGT	ACTGTTAGTG	AGAAATTAAA	ATTCCTTCAG	GAGGATTAAA	CTGCCATTTC	480
AGTTACCCTA	ATTCCAAATG	TTTTGGTGGT	TAGAATCTTC	TTTAATGTTC	TTGAAGAAGT	540
GTTTTATATT	TTCCCATCNA	GATAAATTCT	CTCNCNCCTT	NNTTTTNTNT	CTNNTTTTT	600
AAAACGGANT	CTTGCTCCGT	TGTCCANGCT	GGGAATTTTN	TTTTGGCCAA	TCTCCGCTNC	660
CTTGCAANAA	TNCTGCNTCC	CAAAATTACC	NCCTTTTTCC	CACCTCCACC	CCNNGGAATT	720
ACCTGGAATT	ANAGGCCCCC	NCCCCCCCC	CGGCTAATTT	GTTTTTGTTT	TTAGTAAAAA	780
ACGGGTTTCC	TGTTTTAGTT	AGGATGGCCC	ANNTCTGACC	CCNTNATCNT	CCCCCTCNGC	840
CCTCNAATNT	TNGGNNTANG	GCTTACCCCC	CCCNGNNGTT	TTTCCTCCAT	TNAAATTTTC	900
TNTGGANTCT	TGAATNNCGG	GTTTTCCCTT	TTAAACCNAT	TTTTTTTTTN	NNNCCCCCAN	960
TTTTNCCTCC	CCCNTNTNTA	ANGGGGGTTT	CCCAANCCGG	GTCCNCCCC	ANGTCCCCAA	1020
TTTTTCTCCC	CCCCCCTCTT	TTTTCTTTNC	CCCAAAANTC	CTATCTTTTC	CTNNAAATAT	1080
CNANTNT						1087

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACCAA	GAAATGGGAG	GATTTTAGAG	TGACTGATGA	TTTCTCTATC	ATCTGCAGTT	60
AGTAAACATT	CTCCACAGTT	TATGCAAAAA	GTAACAAAAC	CACTGCAGAT	GACAAACACT	120
AGGTAACACA	CATACTATCT	CCCAAATACC	TACCCACAAG	CTCAACAATT	TTAAACTGTT	180
AGGATCACTG.	GCTCTAATCA	CCATGACATG	AGGTCACCAC	CAAACCATCA	AGCGCTAAAC	240
AGACAGAATG	TTTCCACTCC	TGATCCACTG	TGTGGGAAGA	AGCACCGAAC	TTACCCACTG	300
GGGGGCCTGC	NTCANAANAA	AAGCCCATGC	CCCCGGGTNT	NCCTTTNAAC	CGGAACGAAT	360
NAACCCACCA	TCCCCACANC	TCCTCTGTTC	NTGGGCCCTG	CATCTTGTGG	CCTCNTNTNC	420
TTTNGGGGAN	ACNTGGGGAA	GGTACCCCAT	TTCNTTGACC	CCNCNANAAA	ACCCCNGTGG	480
CCCTTTGCCC	TGATTCNCNT	GGGCCTTTTC	TCTTTTCCCT	TTTGGGTTGT	TTAAATTCCC	540
AATGTCCCCN	GAACCCTCTC	CNTNCTGCCC	AAAACCTACC	TAAATTNCTC	NCTANGNNTT	600
TTCTTGGTGT	TNCTTTTCAA	AGGTNACCTT	NCCTGTTCAN	NCCCNACNAA	AATTTNTTCC	660
NTATNNTGGN	CCCNNAAAAA	NNNATCNNCC	CNAATTGCCC	GAATTGGTTN	GGTTTTTCCT	720
NCTGGGGGAA	ACCCTTTAAA	TTTCCCCCTT	GGCCGGCCCC	CCTTTTTTCC	CCCCTTTNGA	780
AGGCAGGNGG	TTCTTCCCGA	ACTTCCAATT	NCAACAGCCN	TGCCCATTGN	TGAAACCCTT	840
TTCCTAAAAT	NATAAAAAT	CCGGTTNNGG	NNGGCCTCTT	TCCCCTCCNG	GNGGGNNGNG	900
AAANTCCTTA	CCCCNAAAAA	GGTTGCTTAG	CCCCCNGTCC	CCACTCCCCC	NGGAAAAATN	960
AACCTTTTCN	AAAAAAGGAA	TATAANTTTN	CCACTCCTTN	GTTCTCTTCC		1010

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 950 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGAGCTC	GCGGCCGCGA	GCTCTAATAC	GACTCACTAT	AGGGCGTCGA	CTCGATCTCA	60
GCTCACTGCA	ATCTCTGCCC	CCGGGGTCAT	GCGATTCTCC	TGCCTCAGCC	TTCCAAGTAG	120
CTGGGATTAC	AGGCGTGCAA	CACCACACCC	GGCTAATTTT	GTATTTTTAA	TAGAGATGGG	180
GTTTTCCCTT	GTTGGCCANN	ATGGTCTCNA	ACCCCTGACC	TCNNGTGATC	CCCCCNCCCN	240
NGANCTCNNA	CTGCTGGGGA	TNNCCGNNNN	NNNCCTCCCN	NCNCNNNNNN	NCNCNNTCCN	300
TNNTCCTTNC	ТСИМИМИМИ	CNNTCNNTCC	NNCTTCTCNC	CNNNTNTTNT	CNNCNNCCNN	360
CNNNCCNCNT	NCCCNCNNNT	TCNCNTNCNN	TNTCCNNCNN	NNTCNNCNNN	CNNNNCNTNN	420
CCNNTACNTC	NINNICHNNL	CCNTCTNTNN	CCTCNNCNNT	CNCTNCNCNT	TNTCTCCTCN	480
NTNNNNNICT	CCNNINNTCT	CNTCNCNNCN	TUCCTCUUTU	NCCNCNCCCC	NCCTCNCNNC	540
		NTNCCNTTCN				600
CCNCCMNTTC	CTTNCNCNTN	NNNTNTCNNN	CNCNTCNNTC	NTTTNCTCCT	NNNTCCCNNC	660
TCNNTTCNCC	CNNNTCCNCC	CCCCNCCTNT	CTCTCNCCCN	NTNNNTNTN	NNNCNTCCNC	720
TNTCNCNTTC	NTCNNTNCNT	TNCTNTCNNC	NNCNNTNCNC	TNCCNTNTNT	CTNNNTCNCN	780
TCNCNTNTCN	CCNTCCNTTN	CTNTCTCCTN	TNTCCTTCCC	CTCNCCTNCT	CNTTCNCCNC	840
ССИИТИТИТИ	TUNCUCCUNT	NCTNNNCNNC	CNTCNTTTCN	TCTCTNCTNN	NNNTNNCCTC	900
NNCCCNTNCC	CTNNTNCNCT	NCTNNTACCN	TNCTNCTCCN	TCTTCCTTCC		950

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTAGAGCTC	GCGGCCGCGA	GCTCAATTAA	CCCTCACTAA	AGGGAGTCGA	CTCGATCAGA	60
CTGTTACTGT	GTCTATGTAG	AAAGAAGTAG	ACATAAGAGA	TTCCATTTTG	TTCTGTACTA	120
AGAAAAATTC	TTCTGCCTTG	AGATGCTGTT	AATCTGTAAC	CCTAGCCCCA	ACCCTGTGCT	180
CACAGAGACA	TGTGCTGTGT	TGACTCAAGG	TTCAATGGAT	TTAGGGCTAT	GCTTTGTTAA	240
AAAAGTGCTT	GAAGATAATA	TGCTTGTTAA	AAGTCATCAC	CATTCTCTAA	TCTCAAGTAC	300
CCAGGGACAC	AATACACTGC	GGAAGGCCGC	AGGGACCTCT	GTCTAGGAAA	GCCAGGTATT	360
GTCCAAGATT	TCTCCCCATG	TGATAGCCTG	AGATATGGCC	TCATGGGAAC	GGTAAGACCT	420
GACTGTCCCC	CAGCCCGACA	TCCCCCAGCC	CGACATCCCC	CAGCCCGACA	CCCGAAAAGG	480
GTCTGTGCTG	AGGAAGATTA	NTAAAAGAGG	AAGGCTCTTT	GCATTGAAGT	AAGAAGAAGG	540
CTCTGTCTCC	TGCTCGTCCC	TGGGCAATAA	AATGTCT1GG	TGTTAAACCC	GAATGTATGT	600
TCTACTTACT	GAGAATAGGA	GAAAACATCC	TTAGGGCTGG	AGGTGAGACA	CCCTGGCGGC	660
ATACTGCTCT	TTAATGCACG	AGATGTTTGT	NTAATTGCCA	TCCAGGGCCA	NCCCCTTTCC	720
TTAACTTTTT	ATGANACAAA	AACTTTGTTC	NCTTTTCCTG	CGAACCTCTC	CCCCTATTAN	780
CCTATTGGCC	TGCCCATCCC	CTCCCCAAAN	GGTGAAAANA	TGTTCNTAAA	TNCGAGGGAA	840
TCCAAAACNT	TTTCCCGTTG	GTCCCCTTTC	CAACCCCGTC	CCTGGGCCNN	TTTCCTCCCC	900
AACNTGTCCC	GGNTCCTTCN	TTCCCNCCCC	CTTCCCNGAN	AAAAAACCCC	GTNTGANGGN	960
GCCCCTCAA	ATTATAACCT	TTCCNAAACA	AANNGGTTCN	AAGGTGGTTT	GNTTCCGGTG	1020
CGGCTGGCCT	TGAGGTCCCC	CCTNCACCCC	AATTTGGAAN	CCNGTTTTTT	TTATTGCCCN	1080
NTCCCC						1086

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

NCCNTTTAGA	TGTTGACAAN	NTAAACAACC	Mogmonagan			
AAGCATCCTG		OTTAACAACC	NGCTCAGGCA	GCTGAAAAA	GCCACTGATA	60
ATGGTGTTTA	oeimi chuh	GITTACTGTT	AGATCAGCCT	CATTTGACTT	CCCCTCCCAC	120
	cerioe in		TGACTCAAAC	TCCACTATTC	CTGTTCATGA	180
CTGTCAGGAA	1100/11		TGGCCGACCT	GATCTTCAAA	ATGTGCCCCT	240
AGGAAAGGTG	GATGCCACCG	TGTTCACAGA	CAGTACCNCC		AGGGACTACG	300
AGGGGCCGGT	GCANCTGTTA	CCAAGGAGAC	TNATGTGTTG			
AAACACCTCA	NCNCNNAAGG	CTGAATTGAT	CGCCCTCACT			360
GGGATAT"TAA	CGTTAACACT		ACGCCTTTGC		······································	420
CCATCTACCA	GGAGCGTGGG					480
CATCAAAAGG		CIACICACIC	GGCAGGTGGC	TGTNATCCAC	TGTAAANGGA	540
GATGCTGTGT	MAAACNNGGC	TGTTGCCCGT	GGTAACCANA	AANCTGATCN	NCAGCTCNAA	600
	TGACTTTCAC	TCNCNCCTCT	TÄAAČTTĞCT	GCCCACANTC	TCCTTTCCCA	660
ACCAGATCTG	CCTGACAATC	CCCATACTCA	AAAAAAAAN	AANACTGGCC	CCGAACCCNA	720
ACCAATAAAA	ACGGGGANGG	TNGGTNGANC	NNCCTGACCC	AAAAATAATG	GATCCCCCGG	780
GCTGCAGGAA	TTCAATTCAN	CCTTATCNAT			GGCCNGTNCC	
CATTNCCCCT	NTATTNATTC	TTTNNCCCCC				840
GGAAAACCTG	NCTTACCAAN	TTATCNCCTG	occessen1		CTCGTGAAAG	900
AAAAGCCCNC				TTCCNCGGTN	GNTTANAAAA	960
TTNNTCCTTT			CNGAAAGGNA		CCTTTATTTT	1020
· -		CCCCCTTTTA	CCCAGGCGAA		TTAANAAAA	1080
AAANAGAANG	TTTATTTTTC	CTTNGAACCA	TCCCAATANA	AANCACCCGC	NGCGGAACGG	1140
GGNGGNAGGC	CNCTCACCCC	CTTTNTGTNG	GNGGGNC	* . *		1177
						11//

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs

		TOTO L TICTO L TC				
***	(A) LENGTH:	1146 base	pairs			
	(B) TYPE: r	ucleic acid	•			
• * * * .	(C) STRANDE	DNESS: sinc	ile :			
	(D) TOPOLOG	Y: linear	,			
8 •	. 1					
(xi) S	EQUENCE DES	CRIPTION	EO ID NO.9.		, .	
			.5Q 10 NO.3.		•	
NCCNNTTNNT	GATGTTGTCT	TTTTGGCCTC	ጥርጥጥጥርር አጥአ	COMMOGGG	CTTCAGAGGT	
GAAAAGGGTC	AAAAGGAGCT	GTTGACAGTC	ATCCCACCTC	COCCAR	TCCAGAGGT	60
AGACTCCATC	AGTGAGGTCA	AAGCCTGGGG	CTTTTTCACAC	GGCCAATGTG	TCCAGAGTAC TATGGGTTTT	120
CCAATTATAC	AAGTCAGAAG	. TAGAAAGAAG	CCACAGAG	AAGGGAGGAT	TATGGGTTTT GTGGAGCACT	180
CATCACCCAG	AGGGACTTGT	GCCTCTCTCA	GGACATAAAC	CAGGAAGGGG	GTGGAGCACT TCCTCCCACC	240
ACGGTTGCAA	CCAAGAGGCA	ATGGGTCATG	ACCOMAGNAG	AGGGGCTACT	TCCTCCCACC GAGGAGACAT	300
GGGATGACCC	TAAGGGACTA	CCCTCCTTTT	AGCCTACAGG	GGACATANCC	GAGGAGACAT	360
CCTCTTCTTC	AGAGAGAACC	ACTACACCC	AAGGCGGTGG	GACTGGGTGA	GGGAAACTCT	420
ACACGGTCTG	GCTCAGGAAC	AGTACAGGGC	GAGCTGAACC	GGCTGAAGGT	CGAGGCGAAA	480
ATGGAAGGGG	GCTCAGGAAG	ACCIIGGAAG	TAAAATTATG	AATGGTGCAT	GAATGGAGCC	540
GAAGCCGGGA	TGCTCCTGAC	CAAACICAGC	CATTGATCAA	TGTTAGGGAA	ACTGATCAGG	600
CCTTCAAGGG	ATTTCATTAA	TAACCCGCCA	CACAGCTTGA	ACATTGTGAG	GTTCAGTGAC	660
TCCTTTTTT	GCCACTCCAC	TCCAACTTTTG	GCCATTCTAC	TTTGCNAAAT	TTCCAAAACT	720
GGAAAAGGGG	AGGCCGAATC	CNTANTCCCT	NAAAAACNAA	AAAAAATCTG	CNCCTATTCT	780
CNTTTNTTA	CANCCCTTAC	CAGGCTGGAA	GAAATTTTNC	CTTTTTTTTT	TTTTTGAAGG	840
TTCCAAAAA	ATTGAACCTN	AATTCNCCCC	CCCAAAAAAA	AACCCNCCNG	GGGGGCGGAT	900
TICCHAMAAC	NAATTCCCTT	ACCAAAAAAC	AAAAACCCNC	CCTTNTTCCC	TTCCWGGGT	960
IICIIIIAAI	TAGGGAGAGA	TNAAGCCCCC	CAATTTCCNG	GNCTNCATMM	CTTTCCCCCC	1020
CCCCCATITI	CCNAAACTTT	TTCCCANCNA	GGAANCCNCC	Catherine distribution	CONTRACTOR TO THE PARTY OF THE	1080
NCAACCTTCC	AAACCATTTT	TCCNNAAAAA	NTTTGNTNGG	NGGGAAAAAN	ACCTNNTTTT	1140

ATAGAN	1	14	: €	,

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(2) INFORMATION FOR SEQ ID NO:10:

WO 98/45328

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTCATTGGG TAC	GGGCCCC CTCGAGGTCG	ACGGTATCGA	TAAGCTTGAT	ATCGAATTCC	60
TGCAGCCCGG GGGA	ATCCACT AGTTCTAGAG	TCAGGAAGAA	CCACCAACCT	TCCTGATTTT	120
TATTGGCTCT GAG	TTCTGAG GCCAGTTTTC	TTCTTCTGTT	GAGTATGCGG	GATTGTCAGG	180
CAGATCTGGC TGTG	GGAAAGG AGACTGTGGG	CAGCAAGTTT	AGAGGCGTGA	CTGAAAGTCA	240
CACTGCATCT TGAG	GCTGCTG AATCAGCTTT	CTGGTTACCA	CGGGCAACAG	CCGTGTTTTC	300
CTTTTGATGT CCT	TTACAGT GGATTACAGC	CACCTGCTGA	GGTGAGTAGC	CCACGCTCCT	360
GGTAGATGGC TCC	ACGTACA TGCACAGTAG	CAAAGGCGTA	CCTGCTGTCA	GTGTTAACGT	420
TAATATCCTT ACC	CCATCGG AGAGCCTGAG	TGAGGGCGAT	CAATTCAGCC	CTTTTGTGCT	480
GAGGTGTTTG CTG	GTTAAGC CCTGAACCCA	CAACACATCT	GTCTCCATGG	TAACAGCTGC	540
ACCGG					545

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCTAGGC	TGGGCACAGT	GGCTCATACC	TGTAATCCTG	ACCGTTTCAG	AGGCTCAGGT	60
GGGGGGATCG	CTTGAGCCCA	AGATTTCAAG	ACTAGTCTGG	GTAACATAGT	GAGACCCTAT	120
CTCTACGAAA	AAATAAAA	ATGAGCCTGG	TGTAGTGGCA	CACACCAGCT	GAGGAGGGAG	180
AATCGAGCCT	AGGAGA					196

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTCCTAGGC	TTGGGGGCTC	TGACTAGAAA	TTCAAGGAAC	CTGGGATTCA	AGTCCAACTG	60
TGACACCAAC	TTACACTGTG	GNCTCCAATA	AACTGCTTCT	TTCCTATTCC	CTCTCTATTA	120
AATAAAATAA	GGAAAACGAT	GTCTGTGTAT	AGCCAAGTCA	GNTATCCTAA	AAGGAGATAC	180
TAAGTGACAT	TAAATATCAG	AATGTAAAAC	CTGGGAACCA	GGTTCCCAGC	CTGGGATTAA	240

ACTGACAGCA	AGAAGACTGA	ACAGTACTAC	TGTGAAAAGC	CCGAAGNGGC	AATATGTTCA	300
CTCTACCGTT	GAAGGATGGC	TGGGAGAATG	AATGCTCTGT	CCCCCAGTCC	CAAGCTCACT	360
TACTATACCT	CCTTTATAGC	CTAGGAGA				388

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGTAGTTGC CTATAAT	CAT GTTTCTCATT ATTT	TCACAT TTTATTAACC	AATTTCTGTT	60
TACCCTGAAA AATATGA	AGGG AAATATATGA AACA	GGGAGG CAATGTTCAG	ATAATTGATC	120
ACAAGATATG ATTTCTA	ACAT CAGATGCTCT TTCC	TTTCCT GTTTATTTCC	TTTTTATTTC	180
GGTTGTGGGG TCGAATC	GTAA TAGCTT <mark>TG</mark> TT TCAA	GAGAGA GTTTTGGCAG	TTTCTGTAGC	240
TTCTGACACT GCTCATO	STCT CCAGGCATCT ATTT	GCACTT TAGGAGGTGT	CGTGGGAGAC	300
TGAGAGGTCT ATTTTT	rcca tatttgggca acta	CTA	•	337

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGTAGTTGC	CATACAGTGC	CTTTCCATTT	ATTTAACCCC	CACCTGAACG	GCATAAACTG	60
AGTGTTCAGC	TGGTGTTTTT	TACTGTAAAC	AATAAGGAGA	CTTTGCTCTT	CATTTAAACC	120
AAAATCATAT	TTCATATTTT	ACGCTCGAGG	GTTTTTACCG	${\tt GTTCCTTTTT}$	ACACTCCTTA	180
AAACAGTTTT	TAAGTCGTTT	GGAACAAGAT	ATTTTTTCTT	TCCTGGCAGC	TTTTAACATT	240
ATAGCAAATT	TGTGTCTGGG	GGACTGCTGG	TCACTGTTTC	TCACAGTTGC	AAATCAAGGC	300
ATTTGCAACC	AAGAAAAAA	AATTTTTTTG	TTTTATTTGA	AACTGGACCG	GATAAACGGT	360
GTTTGGAGCG	GCTGCTGTAT	ATAGTTTTAA	ATGGTTTATT	GCACCTCCTT	AAGTTGCACT	420
TATGTGGGGG	GGGGNTTTTG	NATAGAAAGT	NTTTANTCAC	ANAGTCACAG	GGACTTTTNT	480
CTTTTGGNNA	CTGAGCTAAA	AAGGGCTGNT	TTTCGGGTGG	GGGCAGATGA	AGGCTCACAG	540
GAGGCCTTTC	TCTTAGAGGG	GGGAACTNCT	A			571

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION; SEQ ID NO:15:

TATATATTTA	ATAACTTAAA	TATATTTTGA	TCACCCACTG	GGGTGATAAG	ACAATAGATA	60
TAAAAGTATT	TCCAAAAAGC	ATAAAACCAA	AGTATCATAC	CAAACCAAAT	TCATACTGCT	120
TCCCCCACCC	GCACTGAAAC	TTCACCTTCT	AACTGTCTAC	CTAACCAAAT	TCTACCCTTC	180
AAGTCTTTGG	TGCGTGCTCA	CTACTCTTTT	TTTTTTTTT	TTTNTTTTGG	AGATGGAGTC	240
TGGCTGTGCA	GCCCAGGGGT	GGAGTACAAT	GGCACAACCT	CAGCTCACTG	NAACCTCCGC	300
CTCCCAGGTT	CATGAGATTC	TCCTGNTTCA	GCCTTCCCAG	TAGCTGGGAC	TACAGGTGTG	360
CATCACCATG	CCTGGNTAAT	CTTTTTTNGT	TTTNGGGTAG	AGATGGGGGT	TTTACATGTT	420
GGCCAGGNTG	GTNTCGAACT	CCTGACCTCA	AGTGATCCAC	CCACCTCAGG	CTCCCAAAGT	480
GCTAGGATTA	CAGACATGAG	CCACTGNGCC	CAGNCCTGGT	GCATGCTCAC	TTCTCTAGGC	540
AACTACTA						548

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCGTTATG	CACATGCAGA	ATATTCTATC	GGTACTTCAG	CTATTACTCA	TTTTGATGGC	60
GCAATCCGAG	CCTATCCTCA	AGATGAGTAT	TTAGAAAGAA	TTGATTTAGC	GA'TAGACCAA	120
GCTGGTAAGC	ACTCTGACTA	CACGAAATTG	TTCAGATGIG	ATGGATTTAT	GACAGTTGAT	180
CTTTGGAAGA	GATTATTAAG	TGATTATTTT	AAAGGGAATC	CATTAATTCC	AGAATATCTT	240
GGTTTAGCTC	AAGATGATAT	AGAAATAGAA	CAGAAAGAGA	CTACAAATGA	AGATGTATCA	300
CCAACTGATA	TTGAAGAGCC	TATAGTAGAA	AATGAATTAG	CTGCATTTAT	TAGCCTTACA	360
CATAGCGATT	TTCCTGATGA	ATCTTATATT	CAGCCATCGA	CATAGCATTA	CCTGATGGGC	420
AACCTTACGA	ATAATAGAAA	CTGGGTGCGG	GGCTATTGAT	${\tt GAATTCATCC}$	NCAGTAAATT	480
TGGATATNAC	AAAATATAAC	TCGATTGCAT	TTGGATGATG	GAATACTAAA	TCTGGCAAAA	540
${\tt GTAACTTTGG}$	AGCTACTAGT	AACCTCTCTT	TTTGAGATGC	AAAATTTTCT	TTTAGGGTTT	600
CTTATTCTCT	ACTTTACGGA	TATTGGAGCA	TAACGGGA			638

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGATGGAT	GTCGCCGGAG	GCGAGGGGCC	TTATCTGATG	CTCGGCTGCC	TGTTCGTGAT	60
GTGCGCGGCG	ATTGGGCTGT	TTATCTCAAA	CACCGCCACG	GCGGTGCTGA	TGGCGCCTAT	120
TGCCTTAGCG	GCGGCGAAGT	CAATGGGCGT	CTCACCCTAT	CCTTTTGCCA	TGGTGGTGGC	180
GATGGCGGCT	TCGGCGGCGT	TTATGACCCC	GGTCTCCTCG	CCGGTTAACA	CCCTGGTGCT	240
TGGCCCTGGC	AAGTACTCAT	TTAGCGATTT	TGTCAAAATA	GGCGTG		286

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
TCGGTCATAG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA TAGCCTTACA TTTTTATAGC CTCCTCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC CATATCACAC ATAACTGCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACTCCT GTGNCAAGAA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTTGTTC TTTNCTATTN TCACTCTTCA CCTATGACCG AA	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
TCGGTCATAG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC ATTTATGATA AATGGTGGCA GGATTTTAT TATAAACATG TACCCATGCA AATTTCCTAT AACTCTGAGA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTTT TAAAAGCCTA ATTTGCGTAG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA CGTTTCTCTG CCTATGACCG A	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:20: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TACAACGAGG CGACGTCGGT AAAATCGGAC ATGAAGCCAC CGCTGGTCTT TTCGTCCGAG CGATAGGCGC CGGCCAGCCA GCGGAACGGT TGCCCGGATG GCGAAGCGAG CCGGAGTTCT TCGGACTGAG TATGAATCTT GTTGTGAAAA TACTCGCCGC CTTCGTTCGA CGACGTCGCG TCGAAATCTT CGANCTCCTT ACGATCGAAG TCTTCGTGGG CGACGATCGC GGTCAGTTCC GCCCCACCGA AATCATGGTT GAGCCGGATG CTGNCCCCGA AGNCCTCGTT TGTN	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:21:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 208 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

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(D) TOPOLOGY: linear

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:21:
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TTGGTAAAGG	GCATGGACGC	AGACGCCTGA	CGTTTGGCTG	AAAATCTTTC	ATTGATTCGT	60
ATCAATGAAT	AGGAAAATTC	CCAAAGAGGG	AATGTCCTGT	TGCTCGCCAG	TTTTTNTGTT	120
GTTCTCATGG	ANAAGGCAAN	GAGCTCTTCA	GACTATTGGN	ATTNTCGTTC	GGTCTTCTGC	180
CAACTAGTCG	NCTTGCNANG	ATCTTCAT				208

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NCCNTTGAGC	TGAGTGATTG	AGATNTGTAA	TGGTTGTAAG	GGTGATTCAG	GCGGATTAGG	60
GTGGCGGGTC	ACCCGGCAGT	GGGTCTCCCG	ACAGGCCAGC	AGGATTTGGG	GCAGGTACGG	. 120
NGTGCGCATC	GCTCGACTAT	ATGCTATGGC	AGGCGAGCCG	TGGAAGGNGG	ATCAGGTCAC	180
GGCGCTGGAG	CTTTCCACGG	TCCATGNATT	GNGATGGCTG	TTCTAGGCGG	CTGTTGCCAA	240
GCGTGATGGT	ACGCTGGCTG	GAGCATTGAT	TTCTGGTGCC	AAGGTGG		287

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGGTAAAG	GGAGCAAGGA	GAAGGCATGG	AGAGGCTCAN	GCTGGTCCTG	GCCTACGACT	60
GGGCCAAGCT	GTCGCCGGGG	ATGGTGGAGA	ACTGAAGCGG	GACCTCCTCG	AGGTCCTCCG	120
NCGTTACTTC	NCCGTCCAGG	AGGAGGGTCT	TTCCGTGGTC	TNGGAGGAGC	GGGGGAGAA	180
GATNCTCCTC	ATGGTCNACA	TCCC				204

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGATTGGTC	ACGACCGGT	AGAGTGGCAC	CATTGAGGGG	ATATTCAAAA	ATATTATTTT	60
GTCCTAAATG	ATAGTTGCTG	AGTTTTTCTT	TGACCCATGA	GTTATATTGG	AGTTTATTTT	120
TTAACTTTCC	AATCGCATGG	ACATGTTAGA	CTTATTTCT	GTTAATGATT	NCTATTTTTA	180

TTAAATTGGA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG ACATTATAGC TTAGTATGTG ACCA	240 264
(2) INFORMATION FOR SEQ ID NO:25:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 376 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG TGCACCEGCA ATCCCAGCTA CTTGGGAGGT TGAGACACAA GANTCACCTA NATGTGGGAG GTCAAGGTTG CATGAGTCAT GATTGTGCCA CTGCACTCCA GCCTGGGTGA CAGACCGAGA CCCTGCCTCA ANAGANAANG AATAGGAAGT TCAGAAATCN TGGNTGTGGN GCCCAGCAAT CTGCATCTAT NCAACCCCTG CAGGCAANGC TGATGCAGCC TANGTTCAAG AGCTGCTGTT TCTGGAGGCA GCAGTTNGGG CTTCCATCCA GTATCACGGC CACACTCGCA CNAGCCATCT GTCCTCCGTN TGTNAC (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 372 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	60 120 180 240 300 360 376
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG TGCACCTGTA ATCCCAGCTA CTTGGGCGGC TGAGACACAA GAACCACCTA AATGTGGGAG GGTCAAGGTT GCATGAGTCA TGATCGCGCC ACTGCACTCC AGCCTGGGTG ACAGACTGAG ACCCTGCCTC AAAAGAAAAA GAATAGGAAG TTCAGAAACC CTGGGTGTGG NGCCCAGCAA TCTGCATTTA AACAATCCCT GCAGGCAATG CTGATGCAGC CTAAGTTCAA GAGCTGCTGT TCTGGAGGCA GNAGTAAGGG CTTCCATCCA GCATCACGGN CAACACTGCA AAAGCACCTG TCCTCGTTGG TA	60 120 180 240 300 360 372
(2) INFORMATION FOR SEQ ID NO:27:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 477 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TTCTGTCCAC ATCTACAAGT TTTATTTATT TTGTGGGTTT TCAGGGTGAC TAAGTTTTTC CCTACATTGA AAAGAGAAGT TGCTAAAAGG TGCACAGGAA ATCATTTTT TAAGTGAATA TGATAATATG GGTCCGTGCT TAATACAACT GAGACATATT TGTTCTCTGT TTTTTTAGAG	60 120 180

TCACCTCTTA	AAGTCCAATC	CCACAATGGT	GAAAAAAAA	TAGAAAGTAT	TTGTTCTACC	240
TTTAAGGAGA	CTGCAGGGAT	TCTCCTTGAA	AACGGAGTAT	GGAATCAATC	TTAAATAAAT	300
ATGAAATTGG	TTGGTCTTCT	GGGATAAGAA	ATTCCCAACT	CAGTGTGCTG	AAATTCACCT	360
GACTTTTTTT	GGGAAAAAAT	AGTCGAAAAT	GTCAATTTGG	TCCATAAAAT	ACATGTTACT	420
ATTAAAAGAT	ATTTAAAGAC	AAATTCTTTC	AGAGCTCTAA	GATTGGTGTG	GACAGAA	477

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x-i) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTNCAACCT	CTTGANTGTC	AAAAACCTTN	TAGCCTATCT	CTAAAAGCTG	ACTGGTATTC	60
ATTCCAGCAA	AATCCCTCTA	GTTTTTGGAG	TTTCCTTTTA	CTATCTGGGG	CTGCCTGAGC	120
CACAAATGCC	AAATTAAGAG	CATGGCTATT	TTCGGGGGCT	GACAGGTCAA	AAGGGGTGTA	180
AATCCGATAA	CCCTCCTGGA	GGTGCTCTAA	AAACACTCCT	GGTGACTCAT	CATGCCCCTG	240
GACGACTTCA	ATCGNCTTAG	ACAAGTTTAT	AGGTTTCTGG	GCAGCTCCCT	GAATACCCAC	300
GAGGAGATAC	CGGTGGAAAT	CGTCAAAAGT	TOTOCOTOCA	CTTGAGAAAT	TTGGGTCCCA	360
ATTAGGTCCC	AATTGGGTCT	CTAATCACTA	TTCCTCTAGC	TTCCTCCTCC	GGNCTATTGG	420
TTGATGTGAG	GTTGAAGA					438

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAGGGTAC	CAGCCCCAAG	CCTTGACAAC	TTCCATAGGG	TGTCAAGCCT	GTGGGTGCAC	60
AGAAGTCAAA	AATTGAGTTT	TGGGATCCTC	AGCCTAGATT	TCAGAGGATA	TAAAGAAACA	120
CCTAACACCT	AGATATTCAG	ACAAAAGTTT	ACTACAGGGA	TGAAGCTTTC	ACGGAAAACC	180
TCTACTAGGA	AAGTACAGAA	GAGAAATGTG	GGTTTGGAGC	CCCCAAACAG	AATCCCCTCT	240
AGAACACTGC	CTAATGAAAC	TGTGAGAAGA	TGGCCACTGT	CATCCAGACA	CCAGAATGAT	300
AGACCCACCA	AAAACTTATG	CCATATTGCC	TATAAAACCT	ACAGACACTC	AA'TGCCAGCC	360
CCATGAAAAA	AAAACTGAGA	AGAAGACTGT	NCCCTACAAT	GCCACCGGAG	CAGAACTGCC	420
CCAGGCCATG	GAAGCACAGC	TCTTATATCA	ATGTGACCTG	GATGTTGAGA	CATGGAATCC	480
NANGAAATCN	TTTTAANACT	TCCACGGTTN	AATGACTGCC	CTATTANATT	CNGAACTTAN	540
ATCCNGGCCT	GTGACCTCTT	TGCTTTGGCC	ATTCCCCCTT	TTTGGAATGG	CTNTTTTTTT	600
CCCATGCCTG	TNCCCTCTTA					620

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TAGTCTATGC	GCCGGACAGA	GCAGAATTAA	ATTGGAAGTT	GCCCTCCGGA"	CTTTCTACCC	50
ACACTCTTCC	TGAAAAGAGA	AAGAAAAGAG	GCAGGAAAGA	GGTTAGGATT	TCATTTTCAA	120
GAGTCAGCTA	ATTAGGAGAG	CAGAGTTTAG	-ACAGCAGTAG	GCACCCCATG	ATACAAACCA	180
TGGACAAAGT	CCCTGTTTAG	TAACTGCCAG	ACATGATCCT	GCTCAGGTTT	TGAAATCTCT	240
CTGCCCATAA	AAGATGGAGA	GCAGGAGTGC	CATCCACATC	AACACGTGTC	CAAGAAAGAG	300
TCTCAGGGAG	ACAAGGGTAT	CAAAAAACAA	GATTCTTAAT	GGGAAGGAAA	TCAAACCAAA	360
AAATTAGATT	TTTCTCTACA	TATATATAAT	ATACAGATAT	TTAACACATT	ATTCCAGAGG	420
TGGCTCCAGT	CCTTGGGGCT	TGAGAGATGG	TGAAAACTTT	TGTTCCACAT	TAACTTCTGC	480
TCTCAAATTC	TGAAGTATAT	CAGAATGGGA	CAGGCAATGT	TTTGCTCCAC	ACTGGGGCAC	540
AGACCCAAAT	GGTTCTGTGC	CCGAAGAAGA	GAAGCCCGAA	AGACATGAAG	GATGCTTAAG	600
GGGGGTTGGG	AAAGCCAAAT	TGGTANTATC	TTTTCCTCCT	GCCTGTGTTC	CNGAAGTCTC	660
CNCTGAAGGA	ATTCTTAAAA	CCCTTTGTGA	GGAAATGCCC	CCTTACCATG	ACAANTGGTC	720
CCATTGCTTT	TAGGGNGATG	GAAACACCAA	GGGTTTTGAT	CC 5		762

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGTCTATGC	GTGTATTAAC	CTCCCCTCCC	TCAGTAACAA	CCAAAGAGGC	AGGAGCTGTT	60
ATTACCAACC	CCATTTTACA	GATGCATCAA	TAATGACAGA	GAAGTGAAGT	GACTTGCGCA	120
CACAACCAGT	AAATTGGCAG	AGTCAGATTT	GAATCCATGG	AGTCTGGTCT	GCACTTTCAA	180
TCACCGAATA	CCCTTTCTAA	GAAACGTGTG	CTGAATGAGT	GCATGGATAA	ATCAGTGTCT	240
ACTCAACATC	TTTGCCTAGA	TATCCCGCAT	AGACTA			276

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TAGTAGTTGC	CAAATATTTG	AAAATTTACC	CAGAAGTGAT	TGAAAACTTT	TTGGAAACAA	60
AAACAAATAA	AGCCAAAAGG	TAAAATAAAA	ATATCTTTGC	ACTCTCGTTA	TTACCTATCC	120
ATAACTTTTT	CACCGTAAGC	TCTCCTGCTT	GTTAGTGTAG	TGTGGTTATA	TTAAACTTTT	180
TAGTTATTAT	TTTTTATTCA	CTTTTCCACT	AGAAAGTCAT	TATTGATTTA	GCACACATGT	240
TGATCTCATT	TCATTTTTTC	TTTTTATAGG	CAAAATTTGA	TGCTATGCAA	CAAAAATACT	300
CAAGCCCATT	ATCTTTTTTC	CCCCCGAAAT	CTGAAAATTG	CAGGGGACAG	AGGGAAGTTA	360
TCCCATTAAA	AAATTGTAAA	TATGTTCAGT	TTATGTTTAA	AAATGCACAA	AACATAAGAA	420
AATTGTGTTT	ACTTGAGCTG	CTGATTGTAA	${\tt GCAGTTTTAT}$	CTCAGGGGCA	ACTACTA	477

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTAGTTGC	CAATTCAGAT	GATCAGAAAT	GCTGCTTTCC	TCAGCATTGT	CTTGTTAAAC	60
CGCATGCCAT	TTGGAACTTT	GGCAGTGAGA	AGCCAAAAGG	AAGAGGTGAA	TGACATATAT	120
TATATATATA	ATTCAATGAA	AGTAAAATGT	ATATGCTCAT	ATACTTTCTA	GTTATCAGAA	180
TGAGTTAAGC	TTTATGCCAT	TGGGCTGCTG	CATATTTTAA	TCAGAAGATA	AAAGAAAATC	240
TGGGCATTTT	TAGAATGTGA	TACATGTTTT	TTTAAAACTG	TTAAATATA	TTTCGATATT	300
TGTCTAAGAA	CCGGAATGTT	CTTAAAATTT	ACTAAAACAG	TATTGTTTGA	GGAAGAGAAA	360
ACTGTACTGT	TTGCCATTAT	TACAGTCGTA	CAAGTGCATG	TCAAGTCACC	CACTCTCTCA	420
GGCATCAGTA	TCCACCTCAT	AGCTTTACAC	ATTTTGACGG	GGAATATTGC	AGCATCCTCA	480
GGCCTGACAT	CTGGGAAAGG	CTCAGATCCA	CCTACTGCTC	CTTGCTCGTT	GATTTGTTTT	540
AAAATATTGT	GCCTGGTGTC	ACTTTTAAGC	CACAGCCCTG	CCTAAAAGCC	AGCAGAGAAC	600
AGAACCCGCA	CCATTCTATA	GGCAACTACT	A			631

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

,	TAGTAGTTGC	CATCCCATAT	TACAGAAGGC	TCTGTATACA	TGACTTATTT	GGAAGTGATC	60
,	TGTTTTCTCT	CCAAACCCAT	TTATCGTAAT	TTCACCAGTC	TTGGATCAAT	CTTGGTTTCC	120
	ACTGATACCA	TGAAACCTAC	TTGGAGCAGA	CATTGCACAG	TTTTCTGTGG	TAAAAACTAA	180
	AGGTTTATTT	GCTAAGCTGT	CATCTTATGC	TTAGTATTTT	TTTTTTACAG	TGGGGAATTG	240
	CTGAGATTAC	ATTTTGTTAT	TCATTAGATA	CTTTGGGATA	ACTTGACACT	GTCTTCTTTT	300
-	TTTCGCTTTT	AATTGCTATC	ATCATGCTTT	TGAAACAAGA	ACACATTAGT	CCTCAAGTAT	360

AAGAATGGGC AAAG GGGTACTGTG GCTC	TGTTAC GCCTGGTGGT TGTTTC CTTATGTTCT GCACTG TAATCCCAGC CGAAAC CAGCCTGGGC	GTAGTTCTCA ACTTTGGGAA	ATAAAAGATT	GCCAGGGGCC	420 480 540 578
(i) SEQUEN (A) L (B) T (C) S	FOR SEQ ID NO:36 CE CHARACTERISTIC ENGTH: 583 base p YPE: nucleic acid TRANDEDNESS: sing DPOLOGY: linear	S: airs			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGTAGTTGC CTGTA	ATCCC AGCAACTCAG	GAGGCTGGGG	CAGGAGAATC	AGTTGAACCT	60
GGGAGGCAGA AGTTG	TAATT AGCAAAGATC	GCACCATTGC	ACTTCAGCCT	GGGCAACAAG	120
AGTGAGATTC CATCTO	САААА АСААААААА	GAAAAAGAAA	AGAAAAGGAA	AAAACGTATA	180
AACCCAGCCA AAACA	AAATG ATCATTCTTT	TAATAAGCAA	GACTAATTTA	ATGTGTTTAT	240
TTAATCAAAG CAGTTO	GAATC TTCTGAGTTA	TTGGTGAAAA	TACCCATGTA	GTTAATTTAG	300
GGTTCTTACT TGGGT	GAACG TTTGATGTTC	ACAGGTTATA	AAATGGTTAA	CAAGGAAAAT	360
GATGCATAAA GAATC	ГТАТА ААСТАСТААА	AATAAATAA	ATATAAATGG	ATAGGTGCTA	420
TGGATGGAGT TTTTGT	IGTAA TTTAAAATCT	TGAAĠTCATT	TTGGATGCTC	ATTGGTTGTC	480
TGGTAATTTC CATTAC	GGAAA AGGTTATGAT	ATGGGGAAAC	TGTTTCTGGA	AATTGCGGAA	540
TGTTTCTCAT CTGTA	AAATG CTAGTATCTC	AGGGCAACTA	CTA		583

(2) INFORMATION FOR SEQ ID NO:37: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCTACTAG	TCATNTGGAT	TCTATCCATG	GCAGCTAAGC	CTTTCTGAAT	GGATTCTACT	60
GCTTTCTTGT	TCTTTAATCC	AGACCCTTAT	ATATGTTTAT	GTTCACAGGC	AGGGCAATGT	120
TTAGTGAAAA	CAATTCTAAA	TTTTTTTTTT	TGCATTTTCA	TGCTAATTTC	CGTCACACTC	180
CAGCAGGCTT	CCTGGGAGAA	TAAGGAGAAA	TACAGCTAAA	GACATTGTCC	CTGCTTACTT	240
ACAGCCTAAT	GGTATGCAAA	ACCACTTCAA	TAAAGTAACA	GGAAAAGTAC	TAACCAGGTA	300
GAATGGACCA	AAACTGATAT	AGAAAAATCA	GAGGAAGAGA	GGAACAAATA	TTTACTGAGT	360
CCTAGAATGT	ACAAGGCTTT	TTAATTACAT	ATTTTATGTA	AGGCCTGCAA	AAAACAGGTG	420
AGTAATCAAC	ATTTGTCCCA	TTTTACATAT	AAGGAAACTG	AAGCTTAAAT	TGAATAATTT	480
AATGCATAGA	TTTTATAGTT	AGACCATGTT	CAGGTCCCTA	TGTTATACTT	ACTAGCTGTA	540
TGAATATGAG	AAAATAATTT	TGTTATTTTC	TTGGCATCAG	TATTTTCATC	TGCAAAATAA	600
AGCTAAAGTT	ATTTAGCAAA	CAGTCAGCAT	AGTGCCTGAT	ACATAGTAGG	TGCTCCAAAC	660
AIGAITACNC	TANTATTNGG	TATTANAAAA	ATCCAATATA	GGCNTGGATA	AAACCG	716

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTCTGTCCAC	ATATCATCCC	ACTTTAATTG	TTAATCAGCA	AAACTTTCAA	TGAAAAATCA	60
TCCATTTTAA	CCAGGATCAC	ACCAGGAAAC	TGAAGGTGTA	TTTTTTTTA	CCTTAAAAAA	120
AAAAAAAA	ACCAAACAAA	CCAAAACAGA	TTAACAGCAA	AGAGTTCTAA	AAAATTTACA	180
TTTCTCTTAC	AACTGTCATT	CAGAGAACAA	TAGTTCTTAA	GTCTGTTAAA	TCTTGGCATT	240
AACAGAGAAA	CTTGATGAAN	AGTTGTACTT	${\tt GGAATATTGT}$	GGATTTTTTT	TTTTGTCTAA	300
TCTCCCCCTA	TTGTTTTGCC	AACAGTAATT	TAAGTTTGTG	TGGAACATCC	CCGTAGTTGA	360
AGTGTAAACA	ATGTATAGGA	AGGAATATAT	GATAAGATGA	TGCATCACAT	ATGCATTACA	420
TGTAGGGACC	TTCACAACTT	CATGCACTCA	GAAAACATGC	TTGAAGAGGA	GGAGAGGACG	480
GCCCAGGGTC	ACCATCCAGG	TGCCTTGAGG	ACAGAGAATG	CAGAAGTGGC	ACTGTTGAAA	540
TTTAGAAGAC	CATGTGTGAA	TGGTTTCAGG	CCTGGGATGT	TTGCCACCAA	GAAGTGCCTC	600
CGAGAAATTT	CTTTCCCATT	TGGAATACAG	GGTGGCTTGA	TGGGTACGGT	GGGTGACCCA	660
ACGAAGAAAA	TGAAATTCTG	CCCTTTCC				688

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TAGTAGTTGC	CGCNNACCTA	AAANTTGGAA	AGCATGATGT	CTAGGAAACA	TANTAAAATA	60
GGGTATGCCT	ATGTGCTACA	GAGAGATGTT	AGCATTTAAA	GTGCATANTT	TTATGTATTT	120
TGACAAATGC	ATATNCCTCT	ATAATCCACA	ACTGATTACG	AAGCTATTAC	AATTAAAAAG	180
TTTGGCCGGG	CGTGGTGGGC	GGTGGCTGAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	240
GGCACGCGGA	TCACGAGGTC	GGGAGTTCAA	GACCATCCTG	GCTAACACGG	TGAAAGTCCA	300
TCTCTACTAA	AAATACGAAA	AAATTACCCC	GGCGTGGTGG	CGGGCGCCTG	TAGTCCCAGC	360
TACTCCGGAG	GCTGAGGCAG	GAGAATGGCG	TGAACCCAGG	ACACGGAGCT	TGCAGTGTGC	420
CAACATCACG	TCACTGCCCT	CCAGCCTGGG	GGACAGGAAC	AAGANTCCCG	TCCTCANAAA	480
AGAAAAATAC	TACTNATANT	TTCNACTTTA	TTTTAANTTA	CACAGAACTN	CCTCTTGGTA	540
		CCCACCTCCT				585

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCTGTCCACA	CCAATCTTAG	AAGCTCTGAA	AAGAATTTGT	CTTTAAATAT	CTTTTAATAG	60
TAACATGTAT	TTTATGGACC	AAATTGACAT	TTTCGACTGT	TTTTTCCAAA	AAAGTCAGGT	120

GAATTTCAGC	ACACTGAGTT	GGGAATTTCT	TATCCCAGAA	GACCAACCAA	TTTCATATTT	180
ATTTAAGATT	GATTCCATAC	TCCGTTTTCA	AGGAGAATCC	CTGCAGTCTC	CTTAAAGGTA	240
GAACAAATAC	TTCCTATTTT	TTTTTCACCA	TTGTGGGATT	GGACTTTAAG	AGGTGACTCT	300
AAAAAAACAG	AGAACAAATA	TGTCTCAGTT	GTATTAAGCA	CGGACCCATA	TTATCATATT	360
CACTTAAAAA	AATGATTTCC	TGTGCACCTT	TTGGCAACTT	CTCTTTTCAA	TGTAGGGAAA	420
AACTTAGTCA	CCCTGAAAAC	CCACAAAATA	AATAAAACTT	GTAGATGTGG	ACAGA	475

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

			* * *			
TAAGAGGGTA	CATCGGGTAA	GAACGTAGGC	ACATCTAGAG	CTTAGAGAAG	TCTGGGGTAG	60
GAAAAAAATC	TAAGTATTTA	TAAGGGTATA	GGTAACATTT	AAAAGTAGGG	CTAGCTGACA	120
TTATTTAGAA	AGAACACATA	CGGAGAGATA	AGGCAAAGG	ACTAAGACCA	GAGGAACACT	180
AATATTTAGT	GATCACTTCC	ATTCTTGGTA	AAAATAGTAA	CTTTTAAGTT	AGCTTCAAGG	240
AAGATTTTTG	GCCATGATTA	GTTGTCAAAA	GTTAGTTCTC	TTGGGTTTAT	ATTACTAATT	300
TTGTTTTAAG	ATCCTTGTTA	GTGCTTTAAT	AAAGTCATGT	TATATCAAAC	GCTCTAAAAC	360
ATTGTAGCAT	GTTAAATGTC	ACAATATACT	TACCATTTGT.	TGTATATGGC	TGTACCCTCT	420
CTA				. 44		423

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

	•**				·-	
TCTCCTAGGC	TAATGTGTGT	GTTTCTGTAA	AAGTAAAAAG	TTAAAAATTT	TAAAAATAGA	60
AAAAAGCTTA	TAGAATAAGA	ATATGAAGAA	AGAAAATATT	TTTGTACATT	TGCACAATGA	120
GTTTATGTTT	TAAGCTAAGT	GTTATTACAA	AAGAGCCAAA	AAGGTTTTAA	AAATTAAAAC	180
GTTTGTAAAG	TTACAGTACC	CTTATGTŤAA	TTTATAATTG	AAGAAAGAAA	AACTTTTTTT	240
TATAAATGTA	GTGTAGCCTA	AGCATACAGT	ATTTATAAAG	TCTGGCAGTG	TTCAATAATG	300
TCCTAGGCCT	TCACATTCAC	TCACTGACTC	ACCCAGAGCA	ACTTCCAGTC	CTGTAAGCTC	360
CATTCGTGGT	AAGTGCCCTA	TACAGGTGCA	CCATTTATTT	TACAGTATTT	TTACTGTACC	420
TTCTCTATGT	TTCCATATGT	TTCGATATAC	AAATACCACT	GGTTACTATN	GCCCNACAGG	480
TAATTCCAGT	AACACGGCCT	GTATACGTCT	GĢTANCCCTA	GNGAAGA		527

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTCAACCT	CGTAGGACAA	CTCTCATATG	CCTGGGCACT	ATTTTTAGGT	TACTACCTTG	60
GCTGCCCTTC	TTTAAGAAAA	AAAAAAGAAG	AAAAAAGAAC	TTTTCCACAA	GTTTCTCTTC	120
CTCTAGTTGG	AAAATTAGAG	AAATCATGTT	TTTAATTTTG	TGTTATTTCA	GATCACAAAT	180
TCAAACACTT	GTAAACATTA	AGCTTCTGTT	CAATCCCCTG	GGAAGAGGAT	TCATTCTGAT	240
ATTTACGGTT	CAAAAGAAGT	TGTAATATTG	TGCTTGGAAC	ACAGAGAACC	AGTTATTAAC	300
TTCCTACTAC	TATTATATAA	TAAATAATAA	С			331

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCTTAGTAG	TTGCCAGGCA	AAATARCGTT	GATTCTCCTC	AGGAGCCACC	CCCAACACCC	60
CTGTTTGCTT	CTAGACCTAT	ACCTAGACTA	AAGTCCCAGC	AGACCCC'I AG	AGGTGAGGTT	120
CAGAGTGACC	CTTGACGAGA	TGTGCTACAC	TAGAAAAGAA	CTGCTTGAGT	TTTCTAATTT	180
ATATAAGCAG	AAATCTGGAG	AAGAGTCATA	GGAATGGATA	TTAAGGGTGT	GAGATAATCC	240
CGGAAGGAAT	ATAGAGTTGG	ATCAGGCTGG	ACTTATTGAT	TTGAACCCAC	TAAGTAGAGA	300
TTCTGCTTTT	GATGTTGCAG	CTCAGGGAGT	TAAAAAAGGT	TTTAATGGTT	CTAATAGTTT	360
ATTTGCTTGG	TTAGCTGAAA	TATGGATAAA	AGATGGCCCA	CTGTGAGCAA	GCTGGAAATG	420
CCTGATCTCT	CTCAGTTTAA	TGTAGAGGAA	GGGATCCAAA	AGTTTAGGGA	GANTTGGATG	480
CTGGRAKTGG	ATTGGTCACT	TTGRGACCTA	CCCWTCCCAG	CTGGGAGGGT	CCAGAAGATA	540
CACCCTTGAC	CAACGCTTTG	CGAAATGGAT	TTGTGATGGC	GGCAACTACT	AA	592

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHAPACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCTTAGTAG	TTGCCATTGC	GAGTGCTTGC	TCAACGAGCG	TTGAACATGG	CGGATTGTCT	60
AGATTCAACG	GATTTGAGTT	TTACCAGCAA	AGCGAACCAA	GCGCGGCCCA	GAGAATTATG	120
GGTTGGTTGG	CTTTGAAAAG	ATGGAAATCC	TGTAGGCCTA	GTCAGAAAAG	CCTTCTTGCA	180
GAACAGTTGG	TTCTCGGGCG	AACGCTCATC	AAGATGCCCA	TTGGAAAGGC	TAGCGTGTAT	240
TTGGGAGAGC	CTGATAGCGT	GTCTTCTGAT	GATGTTTGTG	CTTGGACAGT	GACAAAAGAT	300
ATGCAAAGCA	AGTCCGAACT	AGACGTCAAG	CTTCGTGAGC	AAATTATTGT	AGACTCCTAC	360
TTATACTGTG	AGGAATGATA	GCCAAGGGTG	GGGACTTTAA	GACTAAGGTG	GTTTGTACTT	420
GCGCCGATGA	TCCCAGGCAG	AAAGAMCTGA	TCGCTAGTTT	TATACGGGCA	ACTACTAAGC	480
CGAATTCCAG	CACACTGGCG	GCCGTTACTA	ATTGGATCCG	ANCTCGGTAC	CAGCTTGATG	540
CATASCTTGA	GTTWTCTATA	NTGTCNC				567

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAGCGAAAGA	CCGAGGGCAG	NGNNTANGNG	CGANGAAGCG	GAGAGGGCCA	AAAAGCAACC	60
GCTTTCCCCG	GGGGGTGCCG	ATTCATTAAG	GCAGGTGGAG	GACAGGTTTC	CCGATGGAAG	120
GCGGCAGGGG	CGCAAGCAAT	TAATGTGAGT	AGGCCATTCA	TTÀGCACCCG	GGCTTAACAT	180
TTAAGCTTCG	GGTTGGTATG	TGGTGGGAAT	TGTGAGCGGA	TAACAATTTC	ACACAGGAAA	240
CAGCTATGAC	CATGATTACG	CCAAGCTATT	TAGGTGACAT	TATAGAATAA	CTCAAGTTAT	300
GCATCAAGCT	TGGTACCGAG	TTCGGATCCA	CTAGTAACGG	CCGCCAGTGT	GTGGAATTCG	360
GCTTAGTAGT	TGCCGACCAT	GGAGTGCTAC	CTAGGCTAGA	ATACCTGAGY	TCCTCCCTAG	420
CCTCACTCAC	ATTAAATTGT	ATCTTTTCTA	CATTAGATGT	CCTCAGCGCC	TTATTTCTGC	480
TGGACWATCG	$\mathtt{ATAAATTAAT}$	CCTGATAGGA	TGATAGCAGC	AGATTAATTA	CTGAGAGTAT	540
GTTAATGTGT	CATCCCTCCT	ATATAACGTA	TTTGCATTTT	AATGGAGCAA	TTCTGGAGAT	600
AATCCCTGAA	GGCAAAGGAA	TGAATCTTGA	GGGTGAGAAA	GCCAGAATCA	GTGTCCAGCT	660
GCAGTTGTGG	GAGAAGGTGA	TATTATGTAT	GTCTCAGAAG	TGACACCATA	TGGGCAACTA	720
CTAAGCCCGA	ATTCCAGCAC	ACTGGCGGGC	GTTACTAATG	GATCCGAGCT	CGGTACCAAG	780
CTTGATGCAT	AGCTTGAGTA	TCTATAGTGT	CACTAAATAG	CCTGGCGTTA	TCATGGTCAT	840
AGCTGTTTCC	TGTGTGAAAT	TGTTATCCGC	TCCCAATTCC	CCCCACCATA	CGAGCCGGAA	900
CATAAAGT '			•	•	* , ,	908
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(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGCCAACAAG	GAAAGTTTTA	AATTTCCCCT	TGAGGATTCT	TGGTGATCAT	CAAATTCAGT	60
GGTTTTTAAG	GTTGTTTTCT	GTCAAATAAC	TCTAACTTTA	AGCCAAACAG	TATATGGAAG	120
CACAGATAKA	ATATTACACA	GATAAAAGAG	GAGTTGATCT	AAAGTARAGA	TAGTTGGGGG	180
CTTTAATTTC	TGGAACCTAG	GTCTCCCCAT	CTTCTTCTGT	GCTGAGGAAC	TTCTTGGAAG	240
CGGGGATTCT	AAAGTTCTTT	GGAAGACAGT	TTGAAAACCA	CCATGTTGTT	CTCAGTACCT	300
			GAGAGAAAAG			360
CCCCCCCCCCC	CTTTTTTTT	TTTTAGCTGA	AATAGATACC	CTATGTTNAA	RGAARGGATT	420
ATTATTTACC	ATGCCAYTAR	SCACATGCTC	TTTGATGGGC	NYCTCCSTAC	CCTCCTTAAG	480
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(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGAGGGTAC	CGAGTGGAAT	TTCCGCTTCA	CTAGTCTGGT	GTGGCTAGTC	GGTTTCGTGG	60
TGGCCAACAT	TACGAACTTC	CAACTCAACC	GTTCTTGGAC	GTTCAAGCGG	GAGTACCGGC	120
		TGGCCTTTCT				180
GTATGTTTAT	CAAGATCTTC	TTTACTAACC	CGACCTCTCC	GATTTACCTG	CCCGAGCCGT	240
		ATCCAGTCAC				300
TCGTGACAAT	GCCTATCAAC	TTCGTCGTCA	ATAAGTTGTG	GACCTTCCGA	ACGGTGAAGC	360
ACTCCGAAAA	CGTCCGGTGG	CTGCTGTGCG	GTGACTCCCA	AAATCTTGAT	AACAACAAGG	420
TAACCGAATC	GCGCTAAGGA	ACCCCGCCAT	CTCGGGTACT	CTGCATATGC	GTACCCCTTA	480
		GCGGCCGTTA				540
TGATGCGTAA	CTTGAGTTAT	TCTATAGTGT	CCCTAAAATA	ACCTGGCGTT	A	591

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAGAGGGTAC	CTGCCTTGAA	ATTTAAATGT	CTAAGGAAAR	TGGGAGATGA	TTAAGAGTTG	60
				CTCCTTTCTA		120
AAGAAAGCTG	CTGTGGGGAA	AGGAGGGATA	AATACTGAAG	GGATTTACTA	AACAAATGTC	180
CATCACAGAG	TTTTCCTTTT	TTTTTTTTTG	AGACAGAGTC	TTGCTCTGTC	ACCCAGGCTG	240
GAATGAAGWG	GTATGATCTC	AGTTGAATGC	AACCTCTACC	TCCTAGGTTC	AAGCGATTCT	300
CATGCCTCAG	CCTCCTGAGC	AGCTGGGACT	ATAGGCGCAT	GCTACCATGC	CAGGCTAATT	360
				AGGCAGGTCT	CGAACTCCTG	420
GGCCTCAGAT	GATCTGCCCC	ACCGTACCCT	CTTA			454

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAGAGGGTAC	CAAAAAAAAG	AAAAAGGAAA	AAAAGAAAAA	CAACTTGTAT	AAGGCTTTCT	60
GCTGCATACA	GCTTTTTTTT	TTTAAATAAA	TGGTGCCAAC	AAATGTTTTT	GCATTCACAC	120
					TCCAATAGTG	180
				TCTCATGTAG		240
				TCCGGGGGCC		300
				TGGCTGGGTG		360
				ATAGCCATGA		420
AGCCACTGTT	CATCATTGGC	TGGGACATGC	TGTTACCCTC	יידם	1100101001	463
						402

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid-
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGGÁTTACAG	GACTGAGCCA	CCACGCTCAG	CCTAAGCCTC	60
GATCTACCAC	AGTGATGAGG	GGCTAAAGAG	CACTGCAATT	120
AGATTTATTA	ATTAACAATT	TTTCCTTAGC	ATGTTGGTTC	180
ACTTACTTAG	AAATGAGCTT	TCATTTTAAG	AATTTCATCT	240
' GAGCAGTATG	ACACTATACG	TATTTTATTT	AACTAACCTA	300
AAAGGCTATA	TACATGAATG	TGTATTGTCA	ACTGTAAAGC	360
CAIGAIGICI	TTGAGGTTG	1		399
I	GATCTACCAC GAGATTTATTA GACTTACTTAG GAGCAGTATG AAAAGGCTATA	GATCTACCAC AGTGATGAGG GAGATTTATTA ATTAACAATT GAGTACTTAG AAATGAGCTT GAGCAGTATG ACACTATACG	GATCTACCAC AGTGATGAGG GGCTAAAGAG AGATTTATTA ATTAACAATT TTTCCTTAGC ACTTACTTAG AAATGAGCTT TCATTTTAAG GAGCAGTATG ACACTATACG TATTTTATTT AAAAGGCTATA TACATGAATG TGTATTGTCA	GGGÁTTACAG GACTGAGCCA CCACGCTCAG CCTAAGCCTC GATCTACCAC AGTGATGAGG GGCTAAAGAG CAGTGCAATT AGATTTATTA ATTAACAATT TTTCCTTAGC ATGTTGGTTC ACTTACTTAG AAATGAGCTT TCATTTTATTT AACTAACCTA AAAGGCTATA TACATGAATG TGTATTGTCA ACTGTAAAGC CATGATGTCT TTGAGGTTG

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTCAACCTC AATCAACCTT	CCTXXTTCXT	A A A A M C A M C A	GMM3 3 GM		
	GGIAMIIGAI	AAAATCATCA	CTTAACTTTC	TGATATAATG	60
GCAATAATTA TCTGAGAAAA	AAAAGTGGTG	ΑΑΑΓΑΤΤΔΔΔ	CTTCCATTC	TOTONONAMO	100
TTCAACCAMA -TTTCAACA			CITCCATTIC	ICICAGAAIC	120
TTGAAGGATA TTTGAATAAT	TCAAAAGCGG	AATCAGTAGT	ATCAGCCGAA	GAAACTCACT	180
TAGCTAGAAC CTTCCACCCA	TO COMPONE A CO			O. L. H. C. I. C. I. C. I.	100
TAGCTAGAAC GTTGGACCCA	IGGAICIAAG	TCCCTGCCCT	TCCACTAACC	AGCTGATTGG	240
TTTTGTGTAA ACCTCCTACA	CCCTTCCCCCT	TCCTCCCCTTC	1 mmm		-10
	CGC116GGC1	ragicactic	ATTTGTCAAA	GTAAAGGCTG	300
AAATAGGAAG ATAATGAACC	GTGTCTTTTT	CCTCTCTTTT	CCAMGGAMMA	-	
20111-	GIGICIIIII	GGICICITII	CCATCCATTA	CTCTGATTTT	360
ACAAAGAGGC CTGTATTCCC	CTGGTGAGGT	TG			
		10			392

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTCGGGTGAT GCCTCCTCAG	GCTACAGTGA	A GA CTCCA from	101011100m		
TTTCACATTC CTCTAAAC	CEINCHOIGA	AGACIGGAII	ACAGAAAGGT	GCCAGCGAGA	60
TTTCAGATTC CTGTAAACCT	CTAAAGAAAA	GGAGTCGCGC	CTCAACTGAT	GTAGAAATGA	120
CTAGTTCAGC ATACNGAGAC	ACNTCTGACT	CCGATTCTAG	AGGACTGAGT	GACCTGCAN	179

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

56

(A) LENGTH: 112 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
TTCGGGTGAT GCCTCCTCAG GCTACATCAT NATAGAAGCA AAGTAGAANA ATCNNGTTTG TGCATTTTCC CACANACAAA ATTCAAATGA NTGGAAGAAA TTGGGANAGT AT	60 112
(2) INFORMATION FOR SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
TGAGCTTCCG CTTCTGACAA CTCAATAGAT AATCAAAGGA CAACTTTAAC AGGGATTCAC AAAGGAGTAT ATCCAAATGC CAATAAACAT ATAAAAAGGA ATTCAGCTTC ATCATCATCA GAAGWATGCA AATTAAAACC ATAATGAGAA ACCACTATGT CCCACTAGAA TAGATAAAAT CTTAAAAGAC TGGTAAAACC AAGTGTTGGT AAGGCAAGAG GAGCA	120
(2) INFORMATION FOR SEQ ID NO:56:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 175 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
GCTCCTCTTG CCTTACCAAC ACATTCTCAA AAACCTGTTA GAGTCCTAAG CATTCTCCTG TTAGTATTGG GATTTTACCC CTGTCCTATA AAGATGTTAT GTACCAAAAA TGAAGTGGAG GGCCATACCC TGAGGGAGGG GAGGGATCTC TAGTGTTGTC AGAAGCGGAA GCTCA	60 120 175
(2) INFORMATION FOR SEQ ID NO:57:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	

AGCCATTTAC CACCCATGGA TGAATGGATT TTGTAATTCT AGCTGTTGTA TTTTGTGAAT 60

TTGTTAATTT TGTTGTTTTT CTGTGAAACA CATACATTGG ATATGGGAGG TAAAGGAGTG TCCCAGTTGC TCCTGGTCAC TCCCTTTATA GCCATTACTG TCTTGTTTCT TGTAACTCAG GTTAGGTTTT GGTCTCTTT GCTCCACTGC AAAAAAAAAA	120 180 223
(2) INFORMATION FOR SEQ ID NO:58:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GTTCGAAGGT GAACGTGTAG GTAGCGGATC TCACAACTGG GGAACTGTCA AAGACGAATT AACTGACTTG GATCAATCAA ATGTGACTGA GGAAACACCT GAAGGTGAAG AACATCATCC AGTGGCAGAC ACTGAAAATA AGGAGAATGA AGTTGAAGAG GTAAAAGAGG AGGGTCCAAA AGAGATGACT TTGGATGGGT GGTAAATGGC T	60 120 180 211
(2) INFORMATION FOR SEQ ID NO:59:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GCTCCTCTTG CCTTACCAAC TTTGCACCCA TCATCAACCA TGTGGCCAGG TTTGCAGCCC AGGCTGCACA TCAGGGGACT GCCTCGCAAT ACTTCATGCT GTTGCTGCTG ACTGATGGTG CTGTGACGGA TGTGGAAGCC ACACGTGAGG CTGTGGTGCG TGCCTCGAAC CTGCCCATGT CAGTGATCAT TATGGGTGGT AAATGGCT	60 120 180 208
(2) INFORMATION FOR SEQ ID NO:60:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 171 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
AGCCATTTAC CACCCATACT AAATTCTAGT TCAAACTCCA ACTTCTTCCA TAAAACATCT AACCACTGAC ACCAGTTGGC AATAGCTTCT TCCTTCTTTA ACCTCTTAGA GTATTTATGG TCAATGCCAC ACATTTCTGC AACTGAATAA AGTTGGTAAG GCAAGAGGAG C	60 120 171
(2) INFORMATION FOR SEQ ID NO:61:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 134 base pairs

58

(B) TYPE: nucleic acid

<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
CGGGTGATGC CTCCTCAGGC TTTGGTGTGT CCACTCNACT CACTGGCCTC TTCTCCAGCA ACTGGTGAAN ATGTCCTCAN GAAAANCNCC ACACGCNGCT CAGGGTGGGG TGGGAANCAT CANAATCATC NGGC	60 120 134
(2) INFORMATION FOR SEQ ID NO:62:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
AGAGGGTACA TATGCAACAG TATATAAAGG AAGAAGTGCA CTGAGAGGAA CTTCATCAAG GCCATTTAAT CAATAAGTGA TAGAGTCAAG GCTCAACCCA GGTGTGACGG ATTCCAGGTC CCAAGCTCCT TACTGGTACC CTCTT	60 120 145
(2) INFORMATION FOR SEQ ID NO:63:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xj) SEQUENCE DESCRIPTION: SEQ 1D NO:63:	
TGCACTGAGA GGAATTCAAA GGGTTTATGC CAAAGAACAA ACCAGTCCTC TGCAGCCTAA CTCATTTGTT TTTGGGCTGC GAAGCCATGT AGAGGGCGAT CAGGCAGTAG ATGGTCCCTC CCACAGTCAG CGCCATGGTG GTCCGGTAAA GCATTTGGTC AGGCAGGCCT CGTTTCAGGT AGACGGGCAC ACATCAGCTT TCTGGAAAAA CTTTTGTAGC TCTGGAGCTT TGTTTTTCCC AGCATAATCA TACACTGTGG AATCGGAGGT CAGTTTAGTT GGTAAGGCAA GAGGAGC	60 120 180 240 297
(2) INFORMATION FOR SEQ ID NO:64:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 300 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
GCACTGAGAG GAACTTCCAA TACTATGTTG AATAGGAGTG GTGAGAGAGG GCATCCTTGT	60

CTTGTGCCGG TTTTCAAAGG GAATGCTTCC AGCTTTTGCC CATTCAGTAT AATATTAAAG AATGTTTTAC CATTTTCTGT CTTGCCTGTT TTTCTGTGTT TTTGTTGGTC TCTTCATTCT CCATTTTTAG GCCTTTACAT GTTAGGAATA TATTTCTTTT AATGATACTT CACCTTTGGT ATCTTTTGTG AGACTCTACT CATAGTGTGA TAAGCACTGG GTTGGTAAGG CAAGAGGAGC	120 180 240 300
(2) INFORMATION FOR SEQ ID NO:65:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
GCTCCTCTTG CCTTACCAAC TCACCCAGTA TGTCAGCAAT TTTATCRGCT TTACCTACGA AACAGCCTGT ATCCAAACAC TTAACACACT CACCTGAAAA GTTCAGGCAA CAATCGCCTT CTCATGGGTC TCTCTGCTCC AGTTCTGAAC CTTTCTCTTT TCCTAGAACA TGCATTTARG TCGATAGAAG TTCCTCTCAG TGC	60 120 180 203
(2) INFORMATION FOR SEQ ID NO:66:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 344 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
TACGGGGACC CCTGCATTGA GAAAGCGAGA CTCACTCTGA AGCTGAAATG CTGTTGCCCT TGCAGTGCTG GTAGCAGGAG TTCTGTGCTT TGTGGGCTAA GGCTCCTGGA TGACCCCTGA CATGGAGAAG GCAGAGTTGT GTGCCCCTTC TCATGGCCTC GTCAAGGCAT CATGGACTGC CACACACAAA ATGCCGTTTT TATTAACGAC ATGAAATTGA AGGAGAGAAC ACAATTCACT GATGTGGCTC GTAACCATGG ATATGGTCAC ATACAGAGGT GTGATTATGT AAAGGTTAAT TCCACCCACC TCATGTGGAA ACTAGCCTCA ATGCAGGGGT CCCA	60 120 180 240 300 344
(2) INFORMATION FOR SEQ ID NO:67:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
GCACTGAGAG GAACTTCGTA GGGAGGTTGA ACTGGCTGCT GAGGAGGGGG AACAACAGGG TAACCAGACT GATAGCCATT GGATGGATAA TATGGTGGTT GAGGAGGGAC ACTACTTATA GCAGAGGGTT GTGTATAGCC TGAGGAGGCA TCACCCG	60 120 157

(2) INFORMATION FOR SEQ ID NO:68:

(D) TOPOLOGY: linear

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GCACTGAGAG GAACTTCTAG AAAGTGAAAG TCTAGACATA AAATAAAATA	60 120 137
(2) INFORMATION FOR SEQ ID NO:69:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
CGGGTGATGC CTCCTCAGGC TGTATTTTGA AGACTATCGA CTGGACTTCT TATCAACTGA AGAATCCGTT AAAAATACCA GTTGTATTAT TTCTACCTGT CAAAATCCAT TTCAAATGTT GAAGTTCCTC TCAGTGC	60 120 137
(2) INFORMATION FOR SEQ ID NO:70:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
AGCATGTTGA GCCCAGACAC GCAATCTGAA TGAGTGTGCA CCTCAAGTAA ATGTCTACAC GCTGCCTGGT CTGACATGGC ACACCATCNC GTGGAGGGCA CASCTCTGCT CNGCCTACWA CGAGGGCANT CTCATWGACA GGTTCCACCC ACCAAACTGC AAGAGGCTCA NNAAGTACTR CCAGGGTMYA SGGACMASGG TGGGAYTYCA YCACWCATCT	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:71:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 353 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAGGGTC	TCTATCCACT	CCTAAACCAT	A CA COMOGOO			
99111100010	TOTATCCACT	GCTAAACCAT	ACACC I GGGT	AAACAGGGAC	CATTTAACAT	60
TCCCANCTAA	ATATGCCAAG	TGACTTCACA	TGTTTATCTT	AAAGATGTCC	AAAACGCAAC	120
TGATTTTCTC	CCCTAAACCT	GTGATGGTGG	GATGATTAAN	CCTGAGTGGT	CTACAGCAAG	180
TTAAGTGCAA	GGTGCTAAAT	GAANGTGACC	TGAGATACAG	CATCTACAAC	GCAGTACCTC	
TO A CHICAGO	001		CONOMINENC	CATCIACAAG	GCAGTACCTC	240
ICAACNCAGG	GCAACTTTGC	TTCTCANAGG	GCATTTAGCA	GTGTCTGAAG	TAATTTCTGT	300
ATTACAACTC	ACGGGGGGGG	CCCTCAATAT	CEANEGGAN			
· · · · · · · · · · · · · · · · · · ·	ACGGGGCGGG	GGGIGNATAI	CIANIGGANA	GNAGACCCTA	ACG	353

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

act amakara						
GCACTGAGAG	GAACTTCCAA	TACYATKATC	AGAGTGAACA	RGCARCCYAC	AGAACAGGAG	60
$\lambda \lambda \lambda \lambda TCTTVC$	CA A MOROMOO			ROCHROCIAC	AGAACAGGAG	60
AAAAIGIIIG	CAATCTCTCC	ATCTGACAAA	AGGCTAATAT	CCAGAWTCTA	AWAGGAACTT	120
ΑΑΑΓΑΑΑΤΤΙΤ	λτισησηληλο	7767777777	amariar		······cornicii	120
IN BICIDUITII	ATGAGAAAAG	AACARACAAC	CTCAWCAAAA	AGTGGGTGAA	GGAWATGCTS	180
AAARGAAGAC	ATYTATTCAC	CCACTAAACA	VACCASASA	1000000	TCACTGAWCA	
	MITTATICAG	CCAGTAAACA	IAIGAAAAA	AGGCTCATSA	TCACTGAWCA	240
TTAGAGAAAT	GCAAATCAAA	ACCACAATGA	GATACCATCT	Ay Ances com	AGAAYGGTGA	
		Mechenalda	GATACCATCI	TATRCCAGIT	AGAAYGGTGA	300
TCATTAAAAR	STCAGGAAAC	AACAGATGCT	GGACAAGGTG	TCD		2.42
			00.1012.0010	ICA		343

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCACTGAGAG	GAACTTCAGA	GAGAGAGAGA	GAGTTCCACC	CTGTACTTGG	GGAGAGAAAC	60
AGAAGGTGAG	AAAGTCTTTG	GTTCTGAAGC	AGCTTCTAAG	ATCTTTTCAT	TTGCTTCATT	120
TCAAAGTTCC	CATGCTGCCA	AAGTGCCATC	CTTTGGGGTA	CTGTTTTCTG	AGCTCCAGTG	
ATAACTCATT	TATACAAGGG	AGATACCCAG	AAAAAAACTC	ACCA A AMOUNT	AAAAAGGTGG	180
CTTGAGTTCA	GCCTTANATA	CCATCTTCAA	AMOAGAGAGA	AGCAAAICII	TGTTGGGTGG	240
GAGTGGATAC	AGACCCTAAC	CCATCITGAA	ATGACACAGA	GAAAGAANGA	TGTTGGGTGG	300
CHGIGGAIAG	AGACCCTAAC	G		• • •	•	321

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCACTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCCACC CTGTACTTGG GGAGAGAAAC	60
AGAAGGTGAG AAAGTCTTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT	120
TCAAAGTTCC CATGCTGCCA AAGTGCCATC CTTTGGGGTA CTGTTTTCTG AGCTCCAGTG	
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAAGTG AGCAAATCTT AAAAAGGTGG	180
CTTGAGTTCA GYCTTAAATA CCATCTTGAA ATGAMACAGA GAAAGAAGGA TGTTGGGTGG	240
GAGTGGATAG AGACCCTAAC G	300
	321
(2) INFORMATION FOR SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 317 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
CC) OFC) (I) C C) C C)	
GCACTGAGAG GAACTTCCAC ATGCACTGAG AAATGCATGT TCACAAGGAC TGAAGTCTGG	60
AACTCAGTTT CTCAGTTCCA ATCCTGATTC AGGTGTTTAC CAGCTACACA ACCTTAAGCA	120
AGTCAGATAA CCTTAGCTTC CTCATATGCA AAATGAGAAT GAAAAGTACT CATCGCTGAA	180
TTGTTTTGAG GATTAGAAAA ACATCTGGCA TGCAGTAGAA ATTCAATTAG TATTCATTTT	240
CATTCTTCTA AATTAAACAA ATAGGATTTT TAGTGGTGGA ACTTCAGACA CCAGAAATGG GAGTGGATAG AGACCCT	300
GAGIGGATAG AGACCCT	317
(2) INFORMATION FOR SEQ ID NO:76:	
(i) SEQUENCE CHARACTERISTICS:	
(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 244 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(2) Totobodi. Timear	
(vi) gramma v	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
CGTTAGGGTC TCTATCCACT CCCACTACTG ATCAAACTCT ATTTATTTAA TTATTTTAT	60
CATACTTTAA GTTCTGGGAT ACACGTGCAG CATGCGCAGG TTTGTTGCAT AGGTATACAC	60
TTGCCATGGT GGTTTGCTGC ACCCATCAGT CCATCATCTA CATTAGGTAT TTCTCCTAAT	120
GCTATCCCTC CCCTAGCCCC TTACACCCCC AACAGGCTCT AGTGTGTGAA GTTCCTCTCA	180
GTGC GTGC AGIGIGIGAA GITCCICICA	240
	244
(2) INFORMATION FOR SEQ ID NO:77:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 254 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGTTAGGGTC TCTATCCACT GAAATCTGAA GCACAGGAGG AAGAGAAGCA GTYCTAGTGA

GATGGCAAGT TCWTTTACCA CACTCTTTAA CATTTYGTTT AGTTTTAACC TTTATTTATG GATAATAAAG GTTAATATTA ATAATGATTT ATTTTAAGGC ATTCCCRAAT TTGCATAATT CTCCTTTTGG AGATACCCTT TTATCTCCAG TGCAAGTCTG GATCAAAGTG ATASAMAGAA GTTCCTCTCA GTGC	120 180 240 254
(2) INFORMATION FOR SEQ ID NO:78:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT CCGGATGGT ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTTGCTC TGTTGATGGC CCTGAGGGGA CGCAGGACCC TTATGACCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG ATTGATCCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG CTCCATGAGAT TCCGATGGT TCCAACAGGAT TCCGATGGT TCCAACAGGAT TCCGATGGT TCCAACAGGAT TCCAACAGTAT TCCGATGCT TCCAACAGGAT TCCAACAGTAT TCCAACAGGAT TCCAACAGGAT TCCAACAGTAT TCCAACAGGAT TCCAACAGAGAT TCCAACAGGAT TCCAACAGGAT TCCAACAGAGAT TCCAACAGAGAT TCCAACAGGAT TCCAACAGGAT TCCAACAGGAT TCCAACAGGAT TCCAACAGAGAT TCCAACAGGATAACAGAGAT TCCAACAGAGAT TCCAACAGGAT TCCAACAGAGAT TCCAACAGAGAGAT	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:79:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79: 	
TAAGAGGGTA CCAGCAGAAA GGTTAGTATC ATCAGATAGC ATCTTATACG AGTAATATGC	60
CTGCTATTTG AAGTGTAATT GAGAAGGAAA ATTTTAGCGT CCTCACTGAC CTGCCTGTAG	120
CCCCAGTGAC AGCTAGGATG TGCATTCTCC AGCCATCAAG AGACTGAGTC AAGTTGTTCC	180
TTAAGTCAGA ACAGCAGACT CAGCTCTGAC ATTCTGATTC GAATGACACT GTTCAGGAAT	240
CGGAATCCTG TCGATTAGAC TGGACAGCTT GTGGCAAGTG AATTTGCCTG TAACAAGCCA	300
GATTTTTTAA AATTTATATT GTAAATAATG TGTGTGTG	360
TGTACAGTTA TCTAAGTTAA TTTAAAAGTT GTTTGGTACC CTCTTA	406
(2) INFORMATION FOR SEQ ID NO:80:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 327 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
TTTTTTTTT TTTACTCGGC TCAGTCTAAT CCTTTTTGTA GTCACTCATA GGCCAGACTT AGGGCTAGGA TGATGATTAA TAAGAGGGAT GACATAACTA TTAGTGGCAG GTTAGTTGTT	60
- Interest of the first of the	120

TGTAGGGCTC ATGGTAGGGG TAAAAGGAGG GCAATTTCTA GATCAAATAA TAAGAAGGTA	3.00
ATAGCTACTA AGAAGAATTT TATGGAGAAA GGGACGCGGG CGGGGGATAT AGGGTCGAAG	180
CCGCACTCGT AAGGGGTGGA TTTTTCTATG TAGCCGTTGA GTTGTGGTAG TCAAAATGTA	240
ATAATTATTA GTAGTAAGCC TAGGAGA	300
	327
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 318 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
_(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
TAGTCTATGC GGTTGATTCG GCAATCCATT ATTTGCTGGA TTTTGTCATG TGTTTTGCCA	
ATTGCATTCA TAATTTATTA TGCATTTATG CTTGTTATCT CTAAGTCATG GTATATAATC	60
CATGCTTTTT ATGTTTTGTC TGACATAAAC TCTTATCAGA GCCCTTTGCA CACAGGGATT	120
CAATAAATAT TAACACAGTC TACATTTATT TGGTGAATAT TGCATATCTG CTGTACTGAA	180
AGCACATTAA GTAACAAAGG CAAGTGAGAA GAATGAAAAG CACTACTCAC AACAGTTATC	240
ATGATTGCGC ATAGACTA	300
	318
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 338 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
TCTTCAACCT CTACTCCCAC TAATAGCTTT TTGATGACTT CTAGCAAGCC TCGCTAACCT	60
CGCCTTACCC CCCACTATTA ACCTACTGGG AGAACTCTCT GTGCTAGTAA CCACGTTCTC	120
CTGATCAAAT ATCACTCTCC TACTTACAGG ACTCAACATA CTAGTCACAG CCCTATACTC	180
CCTCTACATA TTTACCACAA CACAATGGGG CTCACTCACC CACCACATTA ACAACATAAA	240
ACCCTCATTC ACACGAGAAA ACACCCTCAT GTTCATACAC CTATCCCCCA TTCTCCTCCT	300
ATCCCTCAAC CCCGACATCA TTACCGGGTT TTCCTCTT	338
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 111 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(2) Torobodi. Iliteat	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
AGCCATTTAC CACCCATCCA CAAAAAAAAA AAAAAAAAA	
ATAGACTTTG AACAAAAAGG AACATTTGCT GGCCTGAGGA GGCATCACCC G	60
GOCCIONOGN GOCKICNOCC G	111

(2)	INFORMATION	FOR	SEQ	ΙD	NO:8	4:	
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCGCGTGATG CCTCCTCAGG					60
AAGGAAGAAA GGAGAAAAA	GGGCATCATC	CCCGTTCCGA	AGGGTCAGGG	AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG					180
CTGGGGAGAG CGAGCCAATC					224

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

(GCACTGAGAG	GAACTTCGTT	GGAAACGGGT	TTTTTTCATG	TAAGGCTAGA	CAGAAGAATT	60
(CTCAGTAACT	TCCTTGTGTT	GTGTGTATTC	AACTCACASA	GTTGAACGAT	CCTTTACACA	120
(GAGCAGACTT	GTAACACTCT	TWTTGTGGAA	TTTGCAAGTG	GAGATTTCAG	SCGCTTTGAA	180
						TCTCAGAAAC	240
•	TCCTTTGTGA	TGTGTGCGTT	CAACTCACAG	AGTTTAACCT	TTCWTTTCAT	AGAAGCAGTT	300
Ž	AGGAAACACT	CTGTTTGTAA	AGTCTGCAAG	TGGÀTAGÀGA	CCCTAACG		348

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCACTCACAC	G 3 3 G 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7					
GCACIGAGAG	GAACTTCYTT	GTGWTGTKTG	YATTCAACTC	ACAGAGTTGA	ASSWTSMTTT	60
ACARAGWKCA	CCCTTKCNNN	CACTCTTTTTT	CIMMON NOTIONO	~	TTTSRRCCRC	
						120
TTTGWGGVCW	WVCKTMCAAM	MCCDUATATIO	TOTAL COLUMN TO A TOTAL OF THE PARTY OF THE	*******		
1110000100	WISKINGAAW	MGGRWATAIC	TICWYAIMRA	AMCTAGACAG	AAKSATTCTC	180
AKAAWSTVVV	VTCTCNUCUC	TCCDTTCAAC	ECA CA CA CUE		KYTSATRGAG	
						240
CAGTTWKGAA	A CTCTMTTTC	TTTCCATTCC	GGA A GMGGA A M	AGAGACCCTA		
CHOTIMOAA	ACICIMITIC	TITGGATICI	GCAAGTGGAT	AGAGACCCTA	ACG	293

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

	(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
CTC	CTAGGCT	10
(2)	INFORMATION FOR SEQ ID NO:88:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
AGT	AGTTGCC	10
(2)	INFORMATION FOR SEQ ID NO:89:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
TTC	CGTTATG C	11
(2)	INFORMATION FOR SEQ ID NO:90:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
TGGI	TAAAGGG	10
(2)	INFORMATION FOR SEQ ID NO:91:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(×i) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
TCGGTCA	TAG	10
(2) INF	ORMATION FOR SEQ ID NO:92:	
(i	SEQUENCE CHARACTERISTICS: (A) LENGTH. 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:92:	
TACAACGA	AGG	10
(2) INFO	DRMATION FOR SEQ ID NO:93:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGGATTGG	TC	10
(2) INFO	RMATION FOR SEQ ID NO:94:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:94:	
CTTTCTAC	сс	10
(2) INFO	RMATION FOR SEQ ID NO:95:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TTTTGGCTCC	10
(2) INFORMATION FOR SEQ ID NO:96:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
GGAACCAATC	10
(2) INFORMATION FOR SEQ ID NO:97:	
(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOFOLOGY: linear	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
TCGATACAGG	10
(2) INFORMATION FOR SEQ ID NO:98:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
GGTACTAAGG	10
(2) INFORMATION FOR SEQ ID NO:99:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
AGTCTATGCG	10

(2)	INFORMATION FOR SEQ ID NO:100:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
CTA	TCCATGG	10
(2)	INFORMATION FOR SEQ ID NO:101:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs. (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
TCT	GTCCACA	10
(2)	INFORMATION FOR SEQ ID NO:102:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO.:102:	
AAGA	AGGGTAC	10
(2)	INFORMATION FOR SEQ ID NO:103:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 103:	
CTTC	CAACCTC	10
(2)	INFORMATION FOR SEQ ID NO:104:	
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
GCTCCTCTTG CCTTACCAAC	20
(2) INFORMATION FOR SEQ ID NO:105:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
GTAAGTCGAG CAGTGTGATG	20
(2) INFORMATION FOR SEQ ID NO:106:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
GTAAGTCGAG CAGTCTGATG	20
(2) INFORMATION FOR SEQ ID NO:107:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
GACTTAGTGG AAAGAATGTA	20
(2) INFORMATION FOR SEQ ID NO:108:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
GTAATTCCGC CAACCGTAGT	20
(2) INFORMATION FOR SEQ ID NO:109:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
ATGGTTGATC GATAGTGGAA	20
(2) INFORMATION FOR SEQ ID NO:110:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
· · · · · · · · · · · · · · · · · · ·	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:	
ACGGGGACCC CTGCATTGAG	20
(2) INFORMATION FOR SEQ ID NO:111:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:	
TATTCTAGAC CATTCGCTAC	20
(2) INFORMATION FOR SEQ ID NO:112:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:	
ACATAACCAC TTTAGCGTTC	20
(2) INFORMATION FOR SEQ ID NO:113:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
CGGGTGATGC CTCCTCAGGC	20
(2) INFORMATION FOR SEQ ID NO:114:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
AGCATGTTGA GCCCAGACAC	20
(2) INFORMATION FOR SEQ ID NO:115:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
GACACCTTGT CCAGCATCTG	20
(2) INFORMATION FOR SEQ ID NO:116:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:	

TACGCTGCAA CACTGTGGAG

(2)	INFO	DRMATION FOR SEQ ID NO:117:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:117:	
CGT	TAGGG	STC TCTATCCACT	20
(2)	_INFO	DRMATION FOR SEQ ID NO:118:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:118:	
AGA	CTGAC'	TTC ATGTCCCCTA	20
(2)	INFO	RMATION FOR SEQ ID NO:119:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:119:	
TCA:		'CG GTGACTCAAG	20
(2)	INFO	PRMATION FOR SEQ ID NO:120:	
		SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:120:	
CAA	SATTC	CA TAGGCTGACC	20
(2)	INFO	RMATION FOR SEC ID NO.121	

	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
ACG:	TACTGGT CTTGAAGGTC	20
(2)	INFORMATION FOR SEQ ID NO:122:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
GAC	GCTTGGC CACTTGACAC	20
(2)	INFORMATION FOR SEQ ID NO:123:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:	
GTA:	ICGACGT AGTGGTCTCC	20
(2)	INFORMATION FOR SEQ ID NO:124:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:	
TAG	TGACATT ACGACGCTGG	20
(2)	INFORMATION FOR SEQ ID NO:125:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:	
CGGGTGATGC CTCCTCAGGC	20
(2) INFORMATION FOR SEQ ID NO:126:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:	
ATGGCTATTT TCGGGGCCTG ACA	23
(2) INFORMATION FOR SEQ ID NO:127:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:	
CCGGTATCTC CTCGTGGGTA TT	22
(2) INFORMATION FOR SEQ ID NO:128:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:	
CTGCCTGAGC CACAAATG	18
(2) INFORMATION FOR SEQ ID NO:129:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129: CCGGAGGAGG AAGCTAGAGG AATA 24 (2) INFORMATION FOR SEQ ID NO:130: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130: TTTTTTTTT TTAG 14 (2) INFORMATION FOR SEQ ID NO:131: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131: Ser Ser Gly Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val 10 Gly Ile (2) INFORMATION FOR SEQ ID NO:132: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132: Gln Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Xaa Ile Glu Val 10 Val Gln Gly His Asp Glu 20 (2) INFORMATION FOR SEQ ID NO:133: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu Ala Tyr Arg Ile Tyr 1 5 10 15

Thr Pro Phe Asp Leu Ser Ala

- (2) INFORMATION FOR SEQ ID NO:134:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Tyr Leu Leu Val Gly Ile Gln Gly Ala 1 5

- (2) INFORMATION FOR SEQ ID NO:135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Ala Ala Gln Lys Pro Ile Asn Leu 1 5

- (2) INFORMATION FOR SEQ ID NO:136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asn Leu Ser Lys Xaa Ile Glu Val Val 1

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu Val Val Gln Gly His Asp Glu Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:138:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENCTH: 9 amino acids
 - (E) TYPE: amino acid
 - (A) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

His Leu Glm Glu Ala Tyr Arg Ile Tyr 1 5

- (2) INFORMATION FOR SEQ ID NO:139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Asn Leu Ala Phe Val Ala Gln Ala Ala 1 5

- (2) INFORMATION FOR SEQ ID NO:140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO.140:

Phe Val Ala Gln Ala Ala Pro Asp Ser 1 5

(2) INFORMATION FCR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGCGGCC	GCGAGCTCAA	TTAACCCTCA	CTAAAGGGAG	TCGACTCGAT	CAGACTGTTA	60
CTGTGTCTAT	GTAGAAAGAA	GTAGACATAA	GAGATTCCAT	TTTGTTCTGT	ACTAAGAAAA	120
ATTCTTCTGC	CTTGAGATGC	TGTTAATCTG	TAACCCTAGC	CCCAACCCTG	TGCTCACAGA	180
GACATGTGCT	GTGTTGACTC	AAGGTTCAAT	GGATTTAGGG	CTATGCTTTG	TTAAAAAAGT	240
GCTTGAAGAT	AATATGCTTG	TTAAAAGTCA	TCACCATTCT	CTAATCTCAA	GTACCCAGGG	300
ACACAATACA	CTGCGGAAGG	CCGCAGGGAC	CTCTGTCTAG	GAAAGCCAGG	TATTGTCCAA	360
GATTTCTCCC	CATGTGATAG	CCTGAGATAT	GGCCTCATGG	GAAGĞG'TAAĞ	ACCTGACTGT	420
			GCCCCAGCCC			480
			TCTTTGCAGT			540
			GTCTTGGTGT			600
			GGCTGGAGGT			660
			AAGTGCACAT			720
			TCACGTTTTC			780
			TCCGAGATGG			840
			GTAGGTCCTC			900
			GTCTCTGTGT			960
			TGTGGAGGGG			1020
			GTGGTGCAGA			1080
			GTCTCCAGCG			1140
			TAAATTTTGA			1200
			TGCTGTGCTT			1260
			TGCACATCCA.			1320
			CTGTGTTGCC			1380
			GCCGTTTCCG			1440
			TGGCCTCCAG			1500
			CCTGCCGGAC			1560
			GGGTGGGAAA			1620
			TCTCATCCGT			1680
			CTGACCCGTA			1740
			AAACGCCTTT			1800
			GGTTGAGGTT			1860
			CCTTTACAAA			1920
			CAGCCAGTTA			1980
			GTCCTAATAG			2040
			TGTAAGGCAC			2100
			ATCTTAGTAG			2160
			CCTTAAATCA			2220
			ATGGACTCCA			2280
GCCCCTTCCT	CAAGGACTTA	ACTTGTGCAA	GCTGACTCCC	AGCACATCCA	AGAATGCAAT	2340
			CCGCAGTTCC			2400
			GTAATAATCT			2460
			TTAACTTTTT			2520
			TCTAAACCAA			2580
			ATTAGCCATC			2640
AATGGACTTT	TAATTTGTCT	CAAAGTGTGG	CGTTTTCTCT	AACTCGCTCA	GGTACGACAT	2700

TTGGAGGCCC	CAGCGAGAAA	CGTCACCGGG	AGAAACGTCA	CCGGGCGAGA	GCCGGGCCCG	2760
					GAAAAAAAAA	2820
					ACCATGCGGG	2880
				CCCGGGGTCA		2940
				GGGTGTCCCT		3000
				TTCTGTTAGA		3060
				CTTGAGTCAG		3120
				TCTCTCTCTC		3180
				CTGGGAAAGA		3240
				GGACAAGGGC		3300
				AGTGGGCCCT		3360
				AGCTCGATCC		3420
				CTAAGGGGGA		3480
GGGCATCTGA	CTGATCCCAT	CACGGGACCC	CCTCCCCTTG	TTTGTCTAAA	AAAAAAAAA	3540
				TGTTTGTTTT		3600
TTCTGTTCGC	TGTCTATTGT	CTTGTTTAGT	GGTTGTCAAG	CTTTTGCATG	TCAGGACGTC	3660
GATATTGCCC	AAGACGTCTG	GGTAAGAACT	TCTGCAAGGT	CCTTAGTGCT	GATTTTTTGT	3720
CACAGGAGG'I	TAAATTTCTC	ATCAATCATT	TAGGCTGGCC	ACCACAGTCC	TGTCTTTTCT	3780
GCCACAAGCA	AGTCAGGTGT	TGTTACGGGA	ATGAGTGTAA	AAAAACATTC	GCCTGATTGG	3840
GATTTCTGGC	ACCATGATGG	TTGTATTTAG	ATTGTCATAC	CCCACATCCA	GGTTGATTGG	3900
ACCTCCTCTA	AACTAAACTG	GTGGTGGGTT	CAAAACAGCC	ACCCTGCAGA	TTTCCTTGCT	3960
CACCTCTTTG	GTCATTCTGT	AACTTTTCCT	GTGCCCTTAA	ATAGCACACT	GTGTAGGGAA	4020
ACCTACCCTC	GTACTGCTTT	ACTTCGTTTA	GATTCTTACT	CTGTTCCTCT	GTGGCTACTC	4080
TCCCATCTTA	AAAACGATCC	AAGTGGTCCT	TTTCCTCCTC	CCTGCCCCCT	ACCCCACACA	4140
TCTCGTTTTC	CAGTGCGACA	GCAAGTTCAG	CGTCTCCAGG	ACTTGGCTCT	GCTCTCACTC	4200
				CCTTTGAGTC		4260
				CACCTAGATC		4320
				TTAAAGCTAC		4380
				GTCATGTTGA		4440
				TGCTGGGTTT		4500
				GGGAAACACT		4560
				TTTTTCTCTC		4620
				ACTCTGCAAA		4680
				CCTCACAATT		4740
				GTTTCCCTAC		4800
				CATGCACCAT		4860
				GACCCTCAGC		4920
				CTCACCCAGT		4980
				CGGCTATGTC		5040
				AAGTAGCCCC		5100
				CCCCCTTCCT		5160
				AATCCTCCCT		5220
				ACACATTGGC		5280
				GAGAGGGAAA		5340
				GAGGAGGAAG		5400
				TTTCTCAAGT		5460
				GGGAGCTGCT		5520
				TGAGTCACCA		5520 5580
				TGACCTGGCA		
				CCCAGATAGT		5640 5700
				AGCTTTTAGA		5700 5760
				CAGCTCAGGC		5760
				TAGATCAGCC		5820
				CTGACTCAAA		5880
						5940
CCICITCAIG	ACIOICAGGA	ACIGITOGAA	ACTACTGAAA	CTGGCCGACC	TGATCTTCAA	6000

AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	GTGTTCACAG	ACAGTAGCAG	CTTCCTCGAG	6060
AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	CAGATGTGTT	GTGGGCTCAG	6120
GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	TCGCCCTCAC	TCAGGCTCTC	6180
CGATGGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	ACGCCTTTGC	TACTGTGCAT	6240
GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	CACCAGGTGG	CTGTAATCCA	6300
CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCGT	GGTAACCAGA	AAGCTGATTC	6360
AGCAGCTCAA	GATGCAGTGT	GACTTTCAGT	CACGCCTCTA	AACTTGCTGC	CCACAGTCTC	6420
CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	ACAGAAGAAG	AAAACTGGCC	6480
TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	$\tt GGTTGGTGGA$	TTCTTCCTGA	CTCTAGAATC	6540
TTCATACCCC	GAACTCTTGG	GAAAACTTTA	ATCAGTCACC	TACAGTCTAC	CACCCATTTA	6600
GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	AGATCCCCCA	TCTTCAAAGC	6660
CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	CAAAAAAGGT	6720
CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	CAGGAGAAAA	GTGGGAAATT	6780
GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	ACTGGTAGAC	6840
ACCTTCTCTG	GATGGACTGA	AGCATTTGCT	ACCAAAAACG	AAACTGTCAA	TATGGTAGTT	6900
AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	AGGGTCTGAT	6960
AATGGACCGG	CCTTCGCCTT	GTCTATAGTT	TAGTCAGTCA	GTAAGGCGTT	AAACATTCAA	7020
TGGAAGCTCC	ATTGTGCCTA	TCGACCCCAG	AGCTCTGGGC	AAGTAGAACG	CATGAACTGC	7080
ACCCTAAAAA	ACACTCTTAC	AAAATTAATC	TTAGAAACCG	GTGTAAATTG	TGTAAGTCTC	7140
CTTCCTTTAG	CCCTACTTAG	AGTAAGGTGC	ACCCCTTACT	GGGCTGGGTT	CTTACCTTTT	7200
GAAATCATGT	ATGGGAGGC	GCTGÇCTĄŢĊ	TTGCCTAAGC	TAAGAGATGC	CCAATTGGCA	7260
AAAATATCAC	AAACTAATTT	ATTACAGTAC	CTACAGTCTC	CCCAACAGGT	ACAAGATATC	7320
ATCCTGCCAC	TTGTTCGAGG	AACCCAŢCĊĊ	AATCCAATTC.	CTGAACAGAC	AGGGCCTGC	7380
CATTCATTCC	CGCCAGGTGA	CCTGTTGTTT	GTTAAAAAGT	TCCAGAGAGA	AGGACTCCCT	7440
CCTGCTTGGA	AGAGACCTCA	CACCGTCATC	ACGATGCCAA	CGGCTCTGAA	GGTGGATGGC	7500
ATTCCTGCGT	GGATTCATCA	CTCCCGCATC	AAAAAGGCCA	ACGGAGCCCA	ACTAGAAACA	7560
TGGGTCCCCA	GGGCTGGGTC	AGGCCCCTTA	AAACTGCACC	TAAGTTGGGT	GAAGCCATTA	7620
GATTAATTCT	TTTTCTTAAT	TTTGTAAAAC	AATGCATAGC	TTCTGTCAAA	CTTATGTATC	7680
TTAAGACTCA	ATATAACCCC	CTTGTTATAA	CTGAGGAATC	AATGATTTGA	TTCCCCAAAA	7740
ACACAAGTGG	GGAATGTAGT	GTCCAACCTG	GTTTTTACTÄ	ACCCTGTTTT	TAGACTCTCC	7800
CTTTCCTTTA	ATCACTCAGC	CTTGTTTCCA	CCTGAATTGA	CTCTCCCTTA	GCTAAGAGCG	7860
CCAGATGGAC	TCCATCTTGG	CTCTTTCACT	GGCAGCCGCT	TCCTCAAGGA	CTTAACTTGT	7920
GCAAGCTGAC	TCCCAGCACA	TCCAAGAATG	CAATTAACTG	ATAAGATACT	GTGGCAAGCT	7980
ATATCCGCAG	TTCCCAGGAA	TTCGTCCAAT	TGATTACACC	CAAAAGCCCC	GCGTCTATCA	8040
				ACGTTCCTGT		8100
CCTTTTAACT	TTTTTGCCTA	CTTTATTTCT	GTAAAATTGT	TTTAACTAGA	CCCCCCTCT	8160
CCTTTCTAAA	CCAAAGTATA	AAAGCAAATC	TAGCCCCTTC	TTCAGGCCGA	GAGAATTTCG	8220
*				TCTTCATGTG	1	8280
				ATTTTCCCCA		8340
TTTAGGGCAC	GTATGTAGAG	TAACTTTTAT	GAAAGAAACC	AGTTAAGGAG	GTTTTGGGAT	8400
				ATTTATTTAT		8460
				TGCGATCTTG		8520
				CTCGAGAGTA		8580
				GTAAAGATGG		8640
	•	·		CTGCCCGCCT		8700
The state of the s		,		ATTTATATGT		8760
				ATATAGGCTG		8820
	• •			TATGTCATCT		8880
				TCCAAATAAC		8940
				TGGCTGTTAC		9000
				ATCATTTTAT		9060
				GGTAGCCCAC		9120
				GGTCTGGGAC		9180
		•		AGAGGGGGTG		9240
•				TTACAGCCTG		9300
				· · · -		-

GGTAGTCAGA	ATTCTTAGGA	GGCACAGGGC	TCCAGGGCAG	ATGCTGAGGG	GTCTTTTATG	9360
${\tt AGGTAGCACA}$	GCAAATCCAC	CCAGGATC				9388

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TGTAAGTCGA	GCAGTGTGAT	GGAAGGAATG	GTCTTTGGAG	AGAGCATATC	CATCTCCTCC	60
TCACTGCCTC	CTAATGTCAT	GAGGTACACT	GAGCAGAATT	AAACAGGGTA	GTCTTAACCA	120
CACTATTTTT	AGCTACCTTG	TCAAGCTAAT	GGTTAAAGAA	CACTTTTGGT	TTACACTTGT	180
TGGGTCATAG	AAGTTGCTTT	CCGCCATCAC	GCAATAAGTT	TGTGTGTAAT	CAGAAGGAGT	240
TACCTTATGG	TTTCAGTGTC	ATTCTTTAGT	TAACTTGGGA	GCTGTGTAAT	TTAGGCTTTG	300
CGTATTATTT	CACTTCTGTT	CTCCACTTAT	GAAGTGATTG	TGTGTTCGCG	TCTGTGTGCG	360
TGCGCATGTG	CTTCCGGCAG	TTAACATAAG	CAAATACCCA	ACATCACACT	GCTCGACTT	419

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGTAAGTCGA	GCAGTGTGAT	GTCCACTGCA	${\tt GTGTGTTGCT}$	GGGAACAGTT	AATGAGCAAA	60
TTGTATACAA	TGGCTAGTAC	ATTGACCGGG	ATTTGTTGAA	GCTGGTGAGT	GTTATGACTT	120
AGCCTGTTAG	ACTAGTCTAT	GCACATGGCT	CTGGTCAACT	ACCGCTCTCT	CATTTCTCCA	180
GATAAATCCC	CCATGCTTTA	TATTCTCTTC	CAAACATACT	ATCCTCATCA	CCACATAGTT	240
CCTTTGTTAA	TGCTTTGTTC	TAGACTTTCC	CTTTTCTGTT	TTCTTATTCA	AACCTATATC	300
TCTTTGCATA	GATTGTAAAT	TCAAATGCCC	TCAGGGTGCA	GGCAGTTCAT	GTAAGGGAGG	360
GAGGCTAGCC	AGTGAGATCT	GCATCACACT	GCTCGACTTA	CA		402

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TCGGGTGATG	CCTCCTCAGG	CCAAGAAGAT	AAAGCTTCAG	ACCCCTAACA	CATTTCCAAA	60
AAGGAAGAAA	GGAGAAAAA	GGGCATCATC	CCCGTTCCGA	AGGGTCAGGG	AGGAGGAAAT	120
TGAGGTGGAT	TCACGAGTTG	CGGACAACTC	CTTTGATGCC	AAGCGAGGTG	CAGCCGGAGA	180

CONTRACTOR OF THE STATE OF THE	22.4
CTGGGGAGAG CGAGCCAATC AGGTTTTGAA GTTCCTCTCA GTGC	224
(2) INFORMATION FOR SEQ ID NO:145:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
AGCCATTTAC CACCCATCCA CAAAAAAAAA AAAAAAAAA	60 111
(2) INFORMATION FOR SEQ ID NO:146:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 585 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:	
TAGCATGTTG AGCCCAGACA CTTGTAGAGA GAGGAGGACA GTTAGAAGAA GAAGAAAAGT	60
TTTTAAATGC TGAAAGTTAC TATAAGAAAG CTTTGGCTTT GGATGAGACT TTTAAAGATG	120
CAGAGGATGC TTTGCAGAAA CTTCATAAAT ATATGCAGGT GATTCCTTAT TTCCTCCTAG	180
AAATTTAGTG ATATTTGAAA TAATGCCCAA ACTTAATTTT CTCCTGAGGA AAACTATTCT	240
ACATTACTTA AGTAAGGCAT TATGAAAAGT TTCTTTTTAG GTATAGTTTT TCCTAATTGG	300
GTTTGACATT GCTTCATAGT GCCTCTGTTT TTGTCCATAA TCGAAAGTAA AGATAGCTGT	360
GAGAAAACTA TTACCTAAAT TTGGTATGTT GTTTTGAGAA ATGTCCTTAT AGGGAGCTCA	420
CCTGGTGGTT TTTAAATTAT TGTTGCTACT ATAATTGAGC TAATTATAAA AACCTTTTTG	480
AGACATATTT TAAATTGTCT TTTCCTGTAA TACTGATGAT GATGTTTTCT CATGCATTTT	540
CTTCTGAATT GGGACCATTG CTGCTGTGTC TGGGCTCACA TGCTA	585
(2) INFORMATION FOR SEQ ID NO:147:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 579 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:	
TAGCATGTTG AGCCCAGACA CTGGGCAGCG GGGGTGGCCA CGGCAGCTCC TGCCGAGCCC	60
AAGCGTGTTT GTCTGTGAAG GACCCTGACG TCACCTGCCA GGCTAGGGAG GGGTCAATGT	120
GGAGTGAATG TTCACCGACT TTCGCAGGAG TGTGCAGAAG CCAGGTGCAA CTTGGTTTGC	180
TTGTGTTCAT CACCCCTCAA GATATGCACA CTGCTTTCCA AATAAAGCAT CAACTGTCAT	240
CTCCAGATGG GGAAGACTTT TTCTCCAACC AGCAGGCAGG TCCCCATCCA CTCAGACACC	300
AGCACGTCCA CCTTCTCGGG CAGCACCACG TCCTCCACCT TCTGCTGGTA CACGGTGATG	360

ATGTCAGCAA AGCCGTTCTG CANGACCAGC TGCCCCGTGT GCTGTGCCAT CTCACTGGCC TCCACCGCGT ACACCGCTCT AGGCCGCGCA TANTGTGCAC AGAANAAATG ATGATCCAGT CCCACAGCCC ACGTCCAAGA NGACTTTATC CGTCAGGGAT TCTTTATTCT GCAGGATGAC CTGTGGTATT AATTGTTCGT GTCTGGGCTC AACATGCTA	420 480 540 579
(2) INFORMATION FOR SEQ ID NO:148:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:	
TGACACCTTG TCCAGCATCT GCAAGCCAGG AAGAGAGTCC TCACCAAGAT CCCCACCCCG TTGGCACCAG GATCTTGGAC TTCCAATCTC CAGAACTGTG AGAAATAAGT ATTTGTCGCT AAATAAATCT TTGTGGTTTC AGATATTTAG CTATAGCAGA TCAGGCTGAC TAAGAGAAAC CCCATAAGAG TTACATACTC ATTAATCTCC GTCTCTATCC CCAGGTCTCA GATGCTGGAC AAGGTGTCA	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:149:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 255 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:	
TGACACCTTG TCCAGCATCT GCTATTTTGT GACTTTTTAA TAATAGCCAT TCTGACTGGT GTGAGATGGT AACTCATTGT GGGTTTGGTC TGCATTTCTC TAATGATCAG TGATATTAAG CTTTTTTTAA ATATGCTTGT TGACCACATG TATATCATCT TTTGAGAAGT GTCTGTTCAT ATCCTTTGCC CACTTTTAA TTTTTTATC TTGTAAATTT GTTTAATTTC CTTACAGATG CTGGACAAGG TGTCA	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:150:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:	
TTACGCTGCA ACACTGTGGA GGCCAAGCTG GGATCACTTC TTCATTCTAA CTGGAGAGGA GGGAAGTTCA AGTCCAGCAG AGGGTGGGTG GGTAGACAGT GGCACTCAGA AATGTCAGCT GGACCCCTGT CCCCGCATAG GCAGGACAGC AAGGCTGTGG CTCTCCAGGG CCAGCTGAAG AACAGGACAC TGTCTCCGCT GCCACAAAGC GTCAGAGACT CCCATCTTTG AAGCACGGCC	60 120 180 240

TTCTTGGTCT TCCTGCACTT CCCTGTTCTG TTAGAGACCT GGTTATAGAC AAGGCTTCTC

CACAGTGTTG CAGCGTAA	318
(2) INFORMATION FOR SEQ ID NO:151:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:	
TNACGCNGCN ACNNTGTAGA GANGGNAAGG CNTTCCCCAC ATTNCCCCTT CATNANAGAA TTATTCNACC AAGNNTGACC NATGCCNTTT ATGACTTACA TGCNNACTNC NTAATCTGTN TCNNGCCTTA AAAGCNNNTC CACTACATGC NTCANCACTG TNTGTGTNAC NTCATNAACT GTCNGNAATA GGGGCNCATA ACTACAGAAA TGCANTTCAT ACTGCTTCCA NTGCCATCNG	60 120 180 240
CGTGTGGCCT TNCCTACTCT TCTTNTATTC CAAGTAGCAT CTCTGGANTG CTTCCCCACT CTCCACATTG TTGCAGCNAT AAT	300 323
(2) INFORMATION FOR SEQ ID NO:152:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:	
TCAAGATTCC ATAGGCTGAC CAGTCCAAGG AGAGTTGAAA TCATGAAGGA GAGTCTATCT GGAGAGAGCT GTAGTTTTGA GGGTTGCAAA GACTTAGGAT GGAGTTGGTG GGTGTGGTTA GTCTCTAAGG TTGATTTTGT TCATAAATTT CATGCCCTGA ATGCCTTGCT TGCCTCACCC TGGTCCAAGC CTTAGTGAAC ACCTAAAAGT CTCTGTCTTC TTGCTCTCCA AACTTCTCCT GAGGATTTCC TCAGATTGTC TACATTCAGA TCGAAGCCAG TTGGCAAACA AGATGCAGTC CAGAGGGTCA G	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:153:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 332 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
CAAGATTCCA TAGGCTGACC AGGAGGCTAT TCAAGATCTC TGGCAGTTGA GGAAGTCTCT TTAAGAAAAT AGTTTAAACA ATTTGTTAAA ATTTTTCTGT CTTACTTCAT TTCTGTAGCA GTTGATATCT GGCTGCCTT TTTATAATGC AGAGTGGGAA CTTTCCCTAC CATGTTTGAT AAATGTTGTC CAGGCTCCAT TGCCAATAAT GTGTTGTCCA AAATGCCTGT TTAGTTTTTA AAGACGGAAC TCCACCCTTT GCTTGGTCTT AAGTATGTAT GGAATGTTAT GATAGGACAT AGTAGTAGCG GTGGTCAGCC TATGGAATCT TG	60 120 180 240 300 332

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TCAAGATTCC	ATAGGCTGAC	CTGGACAGAG	ATCTCCTGGG	TCTGGCCCAG	GACAGCAGGC	60
TCAAGCTCAG	TGGAGAAGGT	TTCCATGACC	CTCAGATTCC	CCCAAACCTT	GGATTGGGTG	120
ACATTGCATC	TCCTCAGAGA	GGGAGGAGAT	GTANGTCTGG	GCTTCCACAG	GGACCTGGTA	180
TTTTAGGATC	AGGGTACCGC	TGGCCTGAGG	CTTGGATCAT	TCANAGCCTG	GGGGTGGAAT	240
${\tt GGCTGGCAGC}$	CTGTGGCCCC	ATTGAAATAG	GCTCTGGGGC	ACTCCCTCTG	TTCCTANTTG	300
AACTTGGGTA	AGGAACAGGA	ATGTGGTCAN	CCTATGGAAT	CTTGA		345

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GACGCTTGGC	CACTTGACAC	ATTAAACAGT	TTTGCATAAT	CACTANCATG	TATTTCTAGT	60
TTGCTGTCTG	CTGTGATGCC	CTGCCCTGAT	TCTCTGGCGT	TAATGATCGC	AAGCATAATC	120
AAACGCTGTT	CTGTTAATTC	CAAGTTATAA	CTGGCATTGA	TTAAAGCATT	ATCTTTCACA	180
ACTAAACTGT	TCTTCATANA	ACAGCCCATA	TTATTATCAA	ATTAAGAGAC	AATGTATTCC	240
AATATCCTTT	ANGGCCAATA	TATTTNATGT	CCCTTAATTA	AGAGCTACTG	TCCGT	295

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GACGCTTGGC	CACTTGACAC	TGCAGTGGGA	AAACCAGCAT	GAGCCGCTGC	CCCCAAGGAA	60
CCTCGAAGCC	CAGGCAGAGG	ACCAGCCATC	CCAGCCTGCA	GGTAAAGTGT	GTCACCTGTC	120
AGGTGGGCTT	GGGGTGAGTG	GGTGGGGGAA	GTGTGTGTGC	AAAGCGGGTG	TNAATGTNTA	180
TGCGTGTGAG	CATGAGTGAT	GGCTACTGTG	ACTGCATGTC	AGGGAGTGTG	AACAAGCGTG	240
CGGGGGTGTG	TGTGCAAGTG	CGTATGCATA	TGAGAATATG	TGTCTGTGGA	TGAGTGCATT	300
TGAAAGTCTG	TGTGTGTGCG	TGTGGTCATG	ANGGTAANTT	ANTGACTGCG	CAGGATGTGT	360
GAGTGTGCAT	GGAACACTCA	NTGTGTGTGT	CAAGTGGCCN	ANCGTC		406

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TGACGCTTGG	CCACTTGACA	CACTAAAGGG	TGTTACTCAT	CACTTTCTTC	TCTCCTCGGT	60
GGCATGTGAG	TGCATCTATT	CACTTGCCAC	TCATTTGTTT	GGCAGTGACT	GTAANCCANA	120
TCTGATGCAT	ACACCAGCTT	CTAAATTGAA	TAAATGTCTC	TAATACTATG	TGCTCACAAT	180
ANGGTANGGG	TGAGGAGAAG	GGGAGAGA				208

- (2) INFORMATION FOR SEQ ID NO:158: W 101 122
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 547 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear (C) STRANDEDNESS: single
 - (xi) SEQUENCE DESCRIPTION: SEQ ID, NO:158:

CTTCAACCTC	CTTCAACCTC	CTTCAACCTC	CTGGATTCAA	ACAATCATCC	CACCTCAGAC	60
TCCTTAGTAG	CTGAGACTAC	AGACTCACGC	CACTACATCT	GGCTAAATTT	TTGTAGAGAT	120
AGGGTTTCAT	CATGTTGCCC	TGGCTGGTCT	CAAACTCCTG	ACCTCAAGCA	ATGTGCCCAC	180
CTCAGCCTCC	CAAAGTGCTG	GGATTACAGG	CATAAGCCAC	CATGCCCAGT	CCATNTTTAA	240
TCTTTCCTAC	CACATTCTTA	CCACACTTTC	TTTTATGTTT	AGATACATAA	ATGCTTACCA	300
TTATGATACA	ATTGCCCACA	GTATTAAGAC	AGTAACATGC	TGCACAGGTT	TGTAGCCTAG	360
GAACAGTAGG	CAATACCACA	TAGCTTAGGT	GTGTGGTAGA	CTATACCATC	TAGGTTTGTG	420
TAAGTTACAC	TTTATGCTGT	TTACACAATG	ACAAAACCAT	CTAATGATGC	ATTTCTCAGA	480
ATGTATCCTT	GTCAGTAAGC	TATGATGTAC	AGGGAACACT	GCCCAAGGAC	ACAGATATTG	540
TACCTGT						547

- (2) INFORMATION FOR SEQ ID NO:159:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GCTCCTCTTG	CCTTACCAAC	TCACCCAGTA	TGTCAGCAAT	TTTATCRGCT	TTACCTACGA	60
AACAGCCTGT	ATCCAAACAC	TTAACACACT	CACCTGAAAA	GTTCAGGCAA	CAATCGCCTT	120
CTCATGGGTC	TCTCTGCTCC	AGTTCTGAAC	CTTTCTCTTT	-TCCTAGAACA	TGCATTTARG	180
TCGATAGAAG	TTCCTCTCAG	TGC	1 8 778			203

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:	
IGTAAGTCGA GCAGTGTGAT GGGTGGAACA GGGTTGTAAG CAGTAATTGC AAACTGTATT IAAACAATAA TAATAATATT TAGCATTTAT AGAGCACTTT ATATCTTCAA AGTACTTGCA AACATTAYCT AATTAAATAC CCTCTCTGAT TATAATCTGG ATACAAATGC ACTTAAACTC AGGACAGGGT CATGAGARAA GTATGCATTT GAAAGTTGGT GCTAGCTATG CTTTAAAAAC CTATACAATG ATGGGRAAGT TAGAGTTCAG ATTCTGTTGG ACTGTTTTTG TGCATTTCAG ITCAGCCTGA TGGCAGAATT AGATCATATC TGCACTCGAT GACTYTGCTT GATAACTTAT CACTGAAATC TGAGTGTTGA TCATCACACT GCTCGACTTA CA (2) INFORMATION FOR SEQ ID NO:161:	60 120 180 240 300 360 402
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 193 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161: AGCATGTTGA GCCCAGACAC TGACCAGGAG AAAAACCAAC CAATAGAAAC ACGCCCAGAC ACTGACCAGG AGAAAAACCA ACCAATAAAA ACAGGCCCGG ACATAAGACA AATAATAAAA ITAGCGGACA AGGACATGAA AACAGCTATT GTAAGAGCGG ATATAGTGGT GTGTGTCTGG GCTCAACATG CTA	60 120 180 193
(2) INFORMATION FOR SEQ ID NO:162: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
IGTTGAGCCC AGACACTGAC CAGGAGAAAA ACCAACCAAT AAAAACAGGC CCGGACATAA GACAAATAAT AAAATTAGCG GACAAGGACA TGAAAACAGC TATTGTAAGA GCGGATATAG IGGTGTGTGT CTGGGCTCAA CATGCTA	60 120 147
(2) INFORMATION FOR SEQ ID NO:163:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 294 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

TAGCATGTTG	AGCCCAGACA	CAAATCTTTC	CTTAAGCAAT	AAATCATTTC	TGCATATGTT	60
TTTAAAACCA	CAGCTAAGCC	ATGATTATTC	AAAAGGACTA	TTGTATTGGG	TATTTTGATT	120
TGGGTTCTTA	TCTCCCTCAC	ATTATCTTCA	TTTCTATCAT	TGACCTCTTA	TCCCAGAGAC	180
TCTCAAACTT	TTATCTTATA	CAAATCACAT	TCTGTCTCAA	AAAATATCTC	ACCCACTTCT	240
CTTCTGTTTC	TGCGTGTGTA	TGTGTGTGTG	TGTGTGTCTG	GGCTCAACAT	GCTA	294

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (P) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CGGGATTGGC	TTTGAGCTGC	AGATGCTGCC	TGTGACCGCA	CCCGGCGTGG	AACAGAAAGC	60
CACCTGGCTG	CAAGTGCGCC	AGAGCCGCCC	TGACTACGTG	CTGCTGTGGG	GCTGGGGCGT	120
GATGAACTCC	ACCGCCCTGA	AGGAAGCCCA	GGCCACCGGA	TACCCCCGCG	ACAAGATGTA	180
${\tt CGGCGTGTGG}$	TGGGCCGGTG	CGGAGCCCGA	TGTGCGTGAC	GTGGGCGAAG	GCGCCAAGGG	240
CTACAACGCG	CTGGCTCTGA	ACGCCTACGG	CACGCAGTCC	AAGGTGATCC	ANGACATCCT	300
GAAACACGTG	CACGACAAGG	GCCAGGGCAC	GGGGCCCAAA	GACGAAGTGG	GCTCGGTGCT	360
GTACACCCGC	GGCGTGATCA	TCCAGATGCT	GGACAAGGTG	TCAATCACTA	AT	412

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TTGACACCTT	GTCCAGCATC	TGCATCTGAT	GAGAGCCTCA	GATGGCTACC	ACTAATGGCA	60
GAAGGCAAAG	GAGAACAGGC	ATTGTATGGC	AAGAAAGGAA	GAAAGAGAGA	GGGGAGAAAG	120
GTGCTAGGTT	CTTTTCAACA	ACCAGTTCTT	GATGGAACTG	AGAGTAAGAG	CTCAAGGCCA	180
GGTGTGGTGA	CTCCAACCAG	TAATCCCAAC	ATTTTAGGAG	GCTGAGGCAG	GCAGATGTCT	240
TGACCCCATG	AGTTTGTGAC	CAGCCTGAAC	AACATCATGA	GACTCCATCT	CTACAATAAT	300
TACAAAAATT	AATCAGGCAT	TGTGGTATGC	CCTGTAGTCC	CAGATGCTGG	ACAAGGTGTC	360
Α						361

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TWGACTGACT	CATGTCCCCT	ACACCCAACT	ATCTTCTCCA	GGTGGCCAGG	CATGATAGAA	60
TCTGATCCTG	ACTTAGGGGA	ATATTTTCTT	TTTACTTCCC	ATCTTGATTC	CCTGCCGGTG	120
AGTTTCCTGG	TTCAGGGTAA	GAAAGGAGCT	CAGGCCAAAG	TAATGAACAA	ATCCATCCTC	180
ACAGACGTAC	AGAATAAGAG	AACWTGGACW	TAGCCAGCAG	AACMCAAKTG	AAAMCAGAAC	240
MCTTAMCTAG	GATRACAAMC	MCRRARATAR	KTGCYCMCMC	WTATAATAGA	AACCAAACTT	300
GTATCTAATT	AAATATTTAT	CCACYGTCAG	GGCATTAGTG	GTTTTGATAA	ATACGCTTTG	360
GCTAGGATTC	CTGAGGTTAG	AATGGAARAA	CAATTGCAMC	GAGGGTAGGG	GACATGAGTC	420
AKTCTAA						427

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AACGTCGCAT	GCTCCCGGCC	GCCATGGCCG	CGGGATAGAC	TGACTCATGT	CCCCTAAGAT	60
AGAGGAGACA	CCTGCTAGCT	GTAAGGAGAA	GATGGTTAGG	TCTACGGAGG	CTCCAGGGTG	120
GGAGTAGTTC	CCTGCTAAGG	GAGGGTAGAC	TGTTCAACCT	GTTCCTGCTC	CGGCCTCCAC	180
TATAGCAGAT	GCGAGCAGGA	GTAGGAGAGA	GCGAGGTAAG	AGTCAGAAGC	TTATGTTGTT	240
TATGCGGGGA	AACGCCRTAT	CGGGGGCAGC	CRAGTTATTA	GGGGACANTR	TAGWYARTCW	300
AGNTAGCATC	CAAAGCGNGG	GAGTTNTCCC	ATATGGTTGG	ACCTGCAGGC	GGCCGCATTA	360
GTGATTAGCA	TGTGAGCCCC	AGACACGCAT	AGCAACAAGG	ACCTAAACTC	AGATCCTGTG	420
CTGATTACTT	AACATGAATT	ATTGTATTTA	TTTAACAACT	TTGAGTTATG	AGGCATAT'IA	480
TTAGGTCCAT	ATTACCTGGA					500

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.168:

TTCATCGCTC	GGTGACTCAA	GCCTGTAATC	CCAGAACTTT	GGGAGGCCGA	GGGGAGCAGA	60
TCACCTGAGG	TTGGGAGTTT	GAGACCAGCC	TGGCCAACAT	GGTGACAACC	CGTCTCTGCT	120
AAAAATACAA	AAATTAGCCA	AGCATGGTGG	CATGCACTIC	TAATCCCAGC	TACTCGGGAG	180
GCTGAGGCAG	GAGAATCACT	TGAGGCCAGG	AGGCAGAGGT	TGCAGTGAGG	CAGAGGTTGA	240
GATCATGCCA	CTGCACTCCA	GCCTGGGCAA	CAGAGTAAGA	CTCCATCTCA	AAAAAAAA	300
AAAAAAAGAA	TGATCAGAGC	CACAAATACA	GAAAACCTTG	AGTCACCGAG	CGATGAAA	358

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TTCTGTCCAC	ACCAATCTTA	GAGCTCTGAA	AGAATTTGTC	TTTAAATATC	TTTTAATAGT	60
AACATGTATT	TTATGGACCA	AATTGACATT	TTCGACTATT	TTTTCCCAAA	AAAAGTCAGG	120
TGAATTTCAG	CACACTGAGT	TGGGAATTTC	TTATCCTAGA	AGWCGGCACG	AGCAATTTCA	180
TATTTATTTA	AGATTGATTC	CATACTCCGT	TTTCAAGGAG	AATCCCTGCA	GTCTCCTTAA	240
AGGTAGAACA	AATACTTTCT	ATTTTTTTTT	CACCATTGTG	GGATTGGACT	TTAAGAGGTG	300
ACTCTAAAAA	AACAGAGAAC	AAATATGTCT	CAGTTGTATT	AAGCACGGAC	CCATATTATC	360
ATATTCACTT	AAAAAAATGA	TTTCCTGTGC	ACCTTTTGGC	AACTTCTCTT	TTCAATGTAG	420
GGAAAAACTT	AGTCACCCTG	AAAACCCACA	AAATAAATAA	AACTTGTAGA	TGTGGGCAGA	480
ARGTTTGGGG	GTGGACATTG	TATGTGTTTA	AATTAAACCC	TGTATCACTG	AGAAGCTGTT	540
GTATGGGTCA	GAGAAAATGA	ATGCTTAGAA	GCTGTTCACA	TCTTCAAGAG	CAGAAGCAAA	600
CCACATGTCT	CAGCTATATT	TTATTTATT	TTTTATGCAT	AAAGTGAATC	ATTTCTTCTG	660
TATTAATTTC	CAAAGGGTTT	TACCCTCTAT	TTAAATGCTT	TGAAAAACAG	TGCATTGACA	720
ATGGGTTGAT	ATTTTTCTTT	AAAAGAAAAA	TATAATTATG	AAAGCCAAGA	TAATCTGAAG	780
CCTGTTTTAT	TTTAAAACTT	TTTATGTTCT	GTGGTTGATG	TTGTTTGTTT	GTTTGTTTCT	840
ATTTTGTTGG	TTTTTTACTT	TGTTTTTTGT	TTTGTTTTGT	TTTGGTTTDG	CATACTACAT	900
GCAGTTTCTT	TAACCAATGT	CTGTTTGGCT	AATGTAATTA	AAGTTGTTAA	TTTATATGAG	960
TGCATTTCAA	CTATGTCAAT	GGTTTCTTAA	TATTTATTGT	GTAGAAGTAC	TGGTAATTTT	1020
TTTATTTACA	ATATGTTTAA	AGAGATAACA	GTTTGATATG	TTTTCATGTG	TTTATAGCAG	1080
AAGTTATTTA	TTTCTATGGC	ATTCCAGCGG	ATATTTTGGT	GTTTGCGAGG	CATGCAGTCA	1140
ATATTTTGTA	CAGTTAGTGG	ACAGTATTCA	GCAACGCCTG	ATAGCTTCTT	TGGCCTTATG	1200
TTAAATAAAA	AGACCTGTTT	GGGATGTAAA	AAAAAAAAA	AAAAAAAAA	AAAAAAAAA	1260
AAAAA				· · · · · · · · · · · · · · · · · · ·	*	1265
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(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TGTAAGTCGA GCAGTG	TGAT GACGATATTC	TTCTTATTAA	TGTGGTAATT	GAACAAATGA	60
TCTGTGATAC TGATCC					120
TAATTGATCC AGAGAA					180
ATTTTTTCTA CAACCA					240
AAGACAAATG TGAAAA					300
ATAATTATCA AACAGO	CACAG CTACTTGCCT	TAATTTTAGA	GTTACTCACA	TTTTGTGTGG	360
AACATCACAC TGCTCC	GACTT ACA				383

(2) INFORMATION FOR SEQ ID NO:171:

í	i)	SEQUENCE	CHARACTERISTICS	

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGGGCACCTT	CAATATCGCA	AGTTAAAAAT	AATGTTGAGT	TTATTATACT	TTTGACCTGT	60
TTAGCTCAAC	AGGGTGAAGG	CATGTAAAGA	ATGTGGACTT	CTGAGGAATT	TTCTTTTAAA	120
AAGAACATAA	TGAAGTAACA	TTTTAATTAC	TCAAGGACTA	CTTTTGGTTG	AAGTTTATAA	180
TCTAGATACC	TCTACTTTTT	GTTTTTGCTG	TTCGACAGTT	CACAAAGACC	TTCAGCAATT	240
TACAGGGTAA	AATCGTTGAA	GTAGTGGAGG	TGAAACTGAA	ATTTAAAATT	ATTCTGTAAA	300
TACTATAGGG	AAAGACGCTG	AGCTTAGAAT	CTTTTGGTTG	TTCATGTGTT	CTGTGCTCTT	360
ATCATCACAC	TGCTCGACTT	ACA				383

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

TCGGGTGATG CCTCCTCAGG	CTTGTCGTTA.	GTGTACACAG	AGCTGCTCAT	GAAGCGACAG	60
CGGCTGCCCC TGGCACTTCA	GAACCTCTTC	CTCTACACTT	TTGGTGCGCT	TCTGAATCTA	120
GGTCTGCATG CTGGCGGCGG	CTCTGGCCCA	GGCCTCCTGG	AAAGTTTCTC	AGGATGGGCA	180
GCACTCGTGG TGCTGAGCCA	GGCACTAAAT	GGACTGCTCA	TGTCTGCTGT	CATGGAGCAT	240
GGCAGCAGCA TCACACGCCT	CTTTGTGGTG	TCCTGCTCGC	TGGTGGTCAA	CGCCGTGCTC	300
TCAGCAGTCC TGCTACGGCT	GCAGCTCACA	GCCGCCTTCT	TCCTGGCCAC	ATTGCTCATT	360
GGCCTGGCCA TGCGCCTGTA	CTATGGCAGC	CGCTAGTCCC	TGACAACTTC	CACCCTGATT	420
CCGGACCCTG TAGATTGGGC	GCCACCACCA	GATCCCCCTC	CCAGGCCTTC	CTCCCTCTCC	480
CATCAGCGGC CCTGTAACAA	GTGCCTTGTG	AGAAAAGCTG	GAGAAGTGAG	GGCAGCCAGG	540
TTATTCTCTG GAGGTTGGTG	GATGAAGGGG	TACCCCTAGG	AGATGTGAAG	TGTGGGTTTG	600
GTTAAGGAAA TGCTTACCAT	CCCCCACCCC	CAACCAAGTT	NTTCCAGACT	AAAGAATTAA	660
GGTAACATCA ATACCTAGGC	CTGAGGAGGC	ATCACCCGA			699

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TCGGGTGATG CCTCCTCAGG	CCAGATCAAA	CTTGGGGTTG	AAAACTGTGC	AAAGAAATCA	60
ATGTCGGAGA AAGAATTTTG	CAAAAGAAAA	ATGCCTAATC	AGTACTAATT	TAATAGGTCA	120

CATTAGCAGT	GGAAGAAGAA	ATGTTGATAT	TTTATGTCAG	CTATTTTATA	ATCACCAGAG	180
TGCTTAGCTT	CATGTAAGCC	ATCTCGTATT	CATTAGAAAT	AAGAACAATT	TTATTCGTCG	240
GAAAGAACTT	TTCAATTTAT	AGCATCTTAA	TTGCTCAGGA	TTTTAAATTT	TGATAAAGAA	300
AGCTCCAC1'T	TTGGCAGGAG	TAGGGGGCAG	GGAGAGAGGA	GGCTCCATCC	ACAAGGACAG	360
AGACACCAGG	GCCAGTAGGG	TAGCTGGTGG	CTGGATCAGT	CACAACGGAC	TGACTTATGC	420
				AACACAAGCT		480
TCACGTTACA	TGTCCTATGT	AGATCAACAG	CAGGTGACTC	AGGGACCCAG	GCTCCATCTC	540
CATATGAGCT	TCCATAGTCA	CCAGGACACG	GGCTCTGAAA	GTGTCCTCCA	TGCAGGGACA	600
				GCCAGAAGTC	ACACTGCAGG	660
GCAGTGCCAT	CCTGCTGTAT	GCCTGAGGAG	GCATCACCCG	Ā		701

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TCGGGTGATG	CCTCCTCANG	CCCCTAAATC	AGAGTCCAGG	GTCAGAGCCA	CAGGAGACAG	60
GGAAAGACAT	AGATTTTAAC	CGGCCCCCTT	CAGGAGATTC	TGAGGCTCAG	TTCACTTTGT	120
TGCAGTTTGA	ACAGAGGCAG	CAAGGCTAGT	GGTTAGGGGC	ACGGTCTCTA	AAGCTGCACT	180
GCCTGGATCT	GCCTCCCAGC	TCTGCCAGGA	ACCAGCTGCG	TGGCCTTGAG	CTGCTGACAC	240
GCAGAAAGCC	CCCTGTGGAC	CCAGTCTCCT	CGTCTGTAAG	ATGAGGACAG	GACTCTAGGA	300
				TCTTGAACTC		360
TTTCCTGAAA	CCTTGTAAAA	${\tt GAAAAAAGTG}$	CTAGCCTGGG	CAACATGGCA	AAACCCTGTC	420
				TGCCTGTAGT		480
				GTGGAGGTTG		540
				ACTCTGTCTC		600
ACAACAACAG	TGAGTGTGCC	TCTGTTTCCG	GGTTGGATGG	GGCACCACAT	TTATGCATCT	660
CTCAGATTTG	GACGCTGCAG	CCTGAGGAGG	CATCACCCGA	•		700
					1	

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TATAGGGCGA ATTGGGCCC	G AGTTGCATGN	TCCCGGCCGC	CATGGCCGCG	GGATTCGGGT	60
GATGCCTCCT CAGGCTTGT	C TGCCACAAGC	TACTTCTCTG	AGCTCAGAAA	GTGCCCCTTG	120
ATGAGGGAAA ATGTCCTAC	T GCACTGCGAA	TTTCTCAGTT	CCATTTTACC	TCCCAGTCCT	180
CCTTCTAAAC CAGTTAATA	A ATTCATTCCA	CAAGTATTTA	CTGATTACCT	GCTTGTGCCA	240
GGGACTATTC TCAGGCTGA					300
GCCAGCTTTA TATTTCAAC	C ATGGCTGGCC	CATCTGAGAG	CATCTCCCCA	CTCTCGCCAA	360
CCTATCGGGG CATAGCCCA	G GGATGCCCCC	AGGCGGCCCA	GGTTAGATGC	GTCCCTTTGG	420
CTTGTCAGTG ATGACATAC	A CCTTAGCTGC	TTAGCTGGTG	CTGGCCTGAG	GAGGCATCAC	480
CCGA	:	8.8			484

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(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCGGGTGATG	CCTCCTCAGG	GCTCAAGGGA	TGAGAAGTGA	CTTCTTTCTG	GAGGGACCGT	60
TCATGCCACC	CAGGATGAAA	ATGGATAGGG	ACCCACTTGG	AGGACTTGCT	GATATGTTTG	120
GACAAATGCC	AGGTAGCGGA	ATTGGTACTG	GTCCAGGAGT	TATCCAGGAT	AGATTTTCAC	180
CCACCATGGG	ACGTCATCGT	TCAAATCAAC	TCTTCAATGG	CCATGGGGGA	CACATCATGC	240
CTCCCACACA	ATCGCAGTTT	GGAGAGATGG	GAGGCAAGTT	TATGAAAAGC	CAGGGGCTAA	300
GCCAGCTCTA	CCATAACCAG	AGTCAGGGAC	TCTTATCCCA	GCTGCAAGGA	CAGTCGAAGG	360
ATATGCCACC	TCGGTTTTCT	AAGAAAGGAC	AGCTTAATGC	AGATGAGATT	AGCCTGAGGA	420
GGCATCACCC	GA					432

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

TAGCATGTTG	AGCCCAGACA	CAGTAGCATT	TGTGCCAATT	TCTGGTTGGA	ATGGTGACAA	60
CATGCTGGAG	CCAAGTGCTA	ACATGCCTTG	GTTCAAGGGA	TGGAAAGTCA	CCCGTAAGGA	120
TGGCAATGCC	AGTGGAACCA	CGCTGCTTGA	GGCTCTGGAC	TGCATCCTAC	CACCAACTCG	180
CCCAACTGAC	AAGCCCTTGC	CCCTGCCTCT	CCAGGATGTC	TACAAAATTG	GTGGTATTGG	240
TACTGTTCCT	GTTGGCCGAG	TGGAGACTGG	TGTTCTCAAA	CCCGGTATGG	TGGTCACCTT	300
TGCTCCAGTC	AACGTTACAA	CGGAAGTAAA	ATCTGTCGAA	ATGCACCATG	AAGCTTTGAG	360
TGAAGCTCTT	CCTGGGGACA	ATGTGGGCTT	CAATGTCAAG	AATGTGTCTG	TCAAGGATGT	420
TCGTCGTGGC	AACGTTGCTG	GTGACAGCAA	AAATGACCCA	CCAATGGAAG	CAGCTGGCTT	480
CACTGCTCAG	GTGATTATCC	TGAACCATCC	AGGCCAAATA	AGTGCCGGCT	ATGCCCCTGT	540
ATTGGATTGC	CACACGGCTC	ACATTGCATG	CAAGTTTGCT	GAGCTGAAGG	AAAAGATTGA	600
TCGCCGTTCT	GGTAAAAAGC	TGGAAGATGG	CCCTAAATTC	TTGAAGTCTG	GTGATGCTGC	660
CATTGTTGAT	ATGGTTCCTG	GCAAGCCCAT	GTGTGTTGAG	AGCTTCTCAG	ACTATCCACC	720
TTTGGGTCGC	TTTGCTGTTC	GTGATATGAG	ACAGACAGTT	GCGGTGGGTG	TCTGGGCTCA	780
ACATGCTA						788

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TAGCATGTTG	AGCCCAGACA	CCTGTGTTTC	TGGGAGCTCT	GGCAGTGGCG	GATTCATAGG	60
CACTTGGGCT	GCACTTTGAA	TGACACACTT	GGCTTTATTA	GATTCACTAG	AAAATTTTT	120
ATTGTTGTTC	GTTTCTTTTC	ATTAAAGGTT	TAATCAGACA	GATCAGACAG	CATAATTTTG	180
TATTTAATGA	CAGAAACGTT	GGTACATTTC	TTCATGAATG	AGCTTGCATT	CTGAAGCAAG	240
AGCCTACAAA	AGGCACTTGT	TATAAATGAA	AGTTCTGGCT	CTAGAGGCCA	GTACTCTGGA	300
GTTTCAGAGC	AGCCAGTGAT	TGTTCCAGTC	AGTGATGCCT	AGTTATATAG	AGGAGGAGTA	360
CACTGTGCAC	TCTTCTAGGT	GTAAGGGTAT	GCAACTTTGG	ATCTTAAAAT	TCTGTACACA	420
TACACACTTT	ATATATATGT	ATCTATGTAT	GAAAACATGA	AATTAGTTTG	TCAAATATGT	480
GTGTGTTTAG	TATTTTAGCT	TAGTGCAACT	ATTTCCACAT	TATTTATTAA	ATTGATCTAA	540
GACACTTTCT	TGTTGACACC	TTGAATATTA	ATGTTCAAGG	GTGCAATGTG	TATTCCTTTA	600
GATTGTTAAA	GCTTAATTAC	TATGATTTGT	AGTAAATTAA	CTTTTAAAAT	GTATTTGAGC	560
CCTTCTGTAG	TGTCGTAGGG	CTCTTACAGG	GTGGGAAAGA	TTTTAATTTT	CCAGTTGCTA	720
ATTGAACAGT	ATGGCCTCAT	TATATATTT	GATTTATAGG	AGTTTGTGTC	TGGGCTCAAC	730
ATGCTA						786

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TAGCATGTTG	AGCCCAGACA	CTGGTTACAA	GACCAGACCT	GCTTCCTCCA	TATGTAAACA	60
GCTTTTAAAA	AGCCAGTGAA	CCTTTTTAAT	ACTTTGGCAA	CCTTCTTTCA	CAGGCAAAGA	120
ACACCCCCAT	CCGCCCCTTG	TTTGGAGTGC	AGAGTTTGGC	TTTGGTTCTT	TĠCCTTGCCT	180
GGAGTATACT	TÇTAATTCCT	GTTGTCCTGC	ACAAGCTGAA	TACCGAGCTA	CCCACCGCCA	240
CCCAGGCCAG	GTTTCCACTC	ATTTATTACT	TTATGTTTCT	GTTCCATTGC	TGGTCCACAG	300
AAATAAGTTT	TCCTTTGGAG	GAATGTGATT	ATACCCCTTT	AATTTCCTCC	TTTTGCTTTT	360
TTTTAATATC	ATTGGTATGT	GTTTGGCCCA	GAGGAAACTG	AAATTCACCA	TCATCTTGAC	420
TGGCAATCCC	ATTACCATGC	TTTTTTTAAA	AAACGTAATT	TTTCTTGCCT	TACATTGGCA	480
GAGTAGCCCT	TCCTGGCTAC	TGGCTTAATG	TAGTCACTCA	GTTTCTAGGT	GGCATTAGGC	540
ATGAGAÇCTG	AAGCACAGAC	TGTCTTACCA	CAAAAGGTGA	CAAGATCTCA	AACCTTAGCC	600
AAAGGGCTAT	GTCAGGTTTC	AATGCTATCT	GCTTCTGTTC	CTGCTCACTG	TTCTGGATTT	660
TGTCCTTCTT	CATCCCTAGC	ACCAGAATTT	CCCAGTCTCC	CTCCCTACCT	TCCCTTGTTT	720
TAATTCTAAT	CTATCAGCAA	AATAACTTTT	CAAATGTTTT	AACCGGTATC	TCCATGTGTC	780
TGGGCTCAAC	ATGCTA					796

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	ACGCCAGGGT	TTTCCCAGTC	ACGACGTTGT	60
AAAACGACGG	CCAGTGAATT	GTAATACGAC	TCACTATAGG	GCGAATTGGG	CCCGACGTCG	120
CATGCTCCCG	GCCGCCATGG	CCGCGGGATA	GCATGTTGAG	CCCAGACACC	TGCAGGTCAT	180
TTGGAGAGAT	TTTTCACGTT	ACCAGCTTGA	TGGTCTTTTT	CAGGAGGAGA	GACACTGAGC	240
ACTCCCAAGG	TGAGGTTGAA	GATTTCCTCT	AGATAGCCGG	ATAAGAAGAC	TAGGAGGGAT	300
GCCTAGAAAA	TGATTAGCAT	GCAAATTTCT	ACCTGCCATT	TCAGAACTGT	GTGTCAGCCC	360
ACATTCAGCT	GCTTCTTGTG	AACTGAAAAG	AGAGAGGTAT	TGAGACTTTT	CTGATGGCCG	420
CTCTAACATT	GTAACACAGT	AATCTGTGTG	TGTGTGGGTG	TGTGTGTGTG	TCTGGGCTCA	480
ACATGCTA						488

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TAGCATGTTG	AGCCCAGACA	CGGCGACGGT	ACCTGATGAG	TGGGGTGATG	GCACCTGTGA	60
AAAGGAGGAA	CGTCATCCCC	CATGATATTG	GGGACCCAGA	TGATGAACC.\.	TGGCTCCGCG	120
TCAATGCATA	TTTAATCCAT	GATACTGCTG	ATTCGAAGGA	CCTGAACCTG	AAGTTTGTGC	180
TGCAGGTTTA	TCGUGACTAT	TACCTCACGG	GTGATCAAAA	CTTCCTGAAG	GACATGTGGC	240
CTGTGTGTCT	AGTAAGGGAT	GCACATGCAG	TGGCCAGTGT	GCCAGGGGTA	TGGTTCGTGT	300
CTGGGCTCAA	CATGCTA				•	317

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TAGCATGTTG	AGCCCAGACA	CTGGCTGTTA	GCCAAATCCT	CTCTCAGCTG	CTCCCTGTGG	60
TTTGGTGACT	CAGGATTACA	GAGGCATCCT	GTTTCAGGGA	ACAAAAAGAT	TTTAGCTGCC	120
AGCAGAGAGC	ACCACATACA	TTAGAATGGT	AAGGACTGCC	ACCTCCTTCA	AGAACAGGAG	180
TGAGGGTGGT	GGTGAATGGG	AATGGAAGCC	TGCATTCCCT	GATGCATTTG	TGCTCTCTCA	240
AATCCTGTCT	TAGTCTTAGG	AAAGGAAGTA	AAGTTTCAAG	GACGGTTCCG	AACTGCTTTT	300
TGTGTCTGGG	CTCAACATGC	TATCCCGCGG	CCATGGCGGC	CGGGAGCATG	CGACGTCGGG	360
CCCAATTCGC	CCTATAGTGA	GTCGTATTAC	AATTCACTGG	CCGTCGTTTT	ACAACGTCGT	420
GACTGGGAAA	ACCCTGGCGT	TACCCAACTT	AATCGCCTTG	CAGCACATCC	CCCTTTCCCA	480
GCTGGCGTAA	TANCGAAAAG	GCCCGCA				507

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATTTACGCT	GCAACACTGT	GGAGGTAGCC	CTGGAGCAAG	CCACCCAMCC	ATGCTTCTGC	
AATCCCCAAA	TCCACCCCC	mammaa.aaa	CIGONOCANG	GCAGGCATGG	ATGCTTCTGC	60
THICCCCAAA	100AGCC1GG	TATTTCAGCC	AGGAATCTGA	GCAGAGCCCC	CTCTAATTGT	120
AGCAATGATA	AGTTATTCTC	TTTGTTCTTC	AACCTTCCAA	TACCCTTCAC	CTTCCAGGGG	
AGTGTCGTTA	ΔΤΟΔΤΤΛΟΛΟ	ССТССТОПО	ACAGTGTTGC	DAULLIJDAG	CTTCCAGGGG	180
	MICHITACAG	CCIGGICICC	ACAGTGTTGC	AGCGTAA		227

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTTTATAAAA CCTG	TGTGGA GCAGATTAAC ATC CCAAATC AATGGCTTCA AAA ACAAAA CTATCAATCAGG	AGTCTAAG GAATAATTTC	GATACTTCAA 12	50 20 30
ATTIGGCCA ATCA	GATATT TTACCTCCAC AGI	IGTTGCAG CGTAA	± 22	25

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid :
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CCCCCCAAGC	2222					
GGCCCGACGT	CGCATGCTCC	CGGCCGCCAT	GGCCGCGGGA	TTCGTTAGGG	TCTCTATCCA	60
CTGGGACCCA	TAGGCTAGTC	AGAGTATTTA	GAGTTGAGTT	CCTTTCTCTCCT	TCCCAGAATT	
TGAAAGAAAA	CCACTCACCT	Camacacac	ONGITORGII	CCITICIGCI	I CCCAGAATT	120
TOTAL	GOAGIGAGGI	GATAGAGCTG	AGAGATCAGA	TTTGCCTCTG	AAGCCTGTTC	180
AAGAIGIAIG	TGCTCAGACC	CCACCACTGG	GGCCTGTGGG	TGAGGTCCTC	CCC A TCCT A TCT	240
TGAATGAATT	GCTGAAGGGG	ACCACTATCC	CAACCAACGG	23.2222	TGGCACTGGC	240
ACACCCCTCA	COTTO	AOCACIAIGC	CAAGGAAGGG	GAACCCATCC	TGGCACTGGC	300
ACAGGGICA	CCTTATCCAG	TGCTCAGTGC	TTCTTTGCTG	CTACCTGGTT	TTCTCTCATA	360
TGTGAGGGCC	AGGTAAGAAG	AAGTGCCCRG	TCTTCTCCCA	CTTTTTTTTTTT	ATCTACCAGT	
AAGTGGCCAA	CTTTTCACAA		TOTIGICGA	GITTTAGAAC	ATCTACCAGT	420
ANOTOGGAA	GITTCACAAA	GCAGCAGCTT	TGTTTTGTGT	ATTTTCACCT	TCAGTTAGAA	480
GAGGAAGGCT	GTGAGATGAA	TGTTAGTTGA	GTGGAAAAGA	CCCCTTAACCT	The same of the sa	
AGACCCTAAC	CAATCACTAC	T077.0110/1	OIGGAAAAGA	CGGGTAAGCT	TAGTGGATAG	540
CCC TAME	GAATCACTAG.	TGCGGCCGCC	TTGCAGGTCG	ACCATATGGG	AGAGCTC	597

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GGCCCGAAGT	TGCATGTTCC	CGGCCGCCAT	GGCCGCGGGA	TTCGTTAGGG	TCTCTATCCA	60
CTACCTAAAA	AATCCCAAAC	ATATAACTGA	ACTCCTCACA	CCCAATTGGA	CCAATCCATC	120
ACCCCAGAGG	CCTACAGATC	CTCCTTTGAT	ACATAAGAAA	ATTTCCCCAA	ACTACCTAAC	180
TATATCATTT	TCCAAGATTT	GTTTTACCAA	ATTTTGATGG	CCTTTCTGAG	CTTGTCAGTG	240
TGAACCACTA	TTACGAACGA	TCGGATATTA	ACTGCCCCTC	ACCGTCCAGG	TGTAGCTGGC	300
AACATCAAGT	GCAGTAAATA	TTCATTAAGT	TTTCACCTAC	TAAGGTGCTT	AAACACCCTA	360
GGGTGCCATG	TCGGTAGCAG	ATCTTTTGAT	TTGTTTTTAT	TTCCCATAAG	GGTCCTGTTC	420
AAGGTCAATC	ATACATGTAG	TGTGAGCAGC	TAGTCACTAT	CGCATGACTT	GGAGGGTGAT	480
AATAGAGGCC	TCCTTTGCTG	TTAAAGAACT	CTTGTCCCAG	CCTGTCAAAG	TGGATAGAGA	540
CCCTAACGAA	TCACTAGTGC	GGCCGCCTGC	AGGTCGACCA	TATGGGAGAG	CTCCCAA	597

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ TD NO:187:

TCGTTAGCGT	CTCTATCCAC	TTGCAGGTAA	AATCCAATCC	TGTGTATATC	TTATAGTCTT	60
CCATATGTAG	TGGTTCAAGA	GACTGCAGTT	CCAGAAAGAC	TAGCCGAGCC	CATCCATGTC	120
TTCCACTTAA	CCCTGCTTTG	GGTTACACAT	CTTAACTTTT	CTGTTCAAGT	TTCTCTGTGT	180
AGTTTATAGC	ATGAGTATTG	GGAWAATGCC	CTGAAACCTG	ACATGAGATC	TGGGAAACAC	240
AAACTTACTC	AATAAGAATT	TCTCCCATAT	TTTTATGATG	GAAAAATTTC	ACATGCACAG	300
AGGAGTGGAT	AGAGACCCTA	ACGA				324

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GCGCGGGGAT	TCGGGGTGAT	ACCTCCTCAT	GCCAAAATAC	AACGTNTAAT	TTCACAACTT	60
GCCTTCCAAT	TTACGCATTT	TCAATTTGCT	CTCCCCATTT	GTTGAGTCAC	AACAAACACC	120
ATTGCCCAGA	AACATGTATT	ACCTAACATG	CACATACTCT	TAAAACTACT	CATCCCTT	178

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TGACACCTTG	TCCAGCATCT	GACACAGTCT	TGGCTCTTGG	AAAATATTGG	ATAAATGAAA	60
ATGAATTTCT	TTAGCAAGTG	GTATAAGCTG	AGAATATACG	TATCACATAT	CCTCATTCTA	120
AGACACATTC	AGTGTCCCTG	AAATTAGAAT	AGGACTTACA	ATAAGTGTGT	TCACTTTCTC	180
		TGGTAGGCCT				240
AAAAAAGCTC	AACATCACTG	ATCATTAGAA	AACTTCCATT	CAAACCCCCA	ATGAGATACC	300
ATCTCATACC	AGTCAGAATG	GCTATTATTA	AAAAGTCAAA	AAATAACAGA	TGCTGGACAA	360
GGTGTCA					•	367

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

				AGATCTTTAT		60
				ATTTACCCAT		120
				ACTGCTCTGG		180
				AACTTCCACT		240
AAACAGATGA	TATATACAAA	TATATAAATG	AATTCAGGTA	GTTTTAAGTA	CGAAAAGAAT	300
AAGAAAGCAG	AGTCATGATT	TANAATGCTG	GAAACAGGGG	CTATTGCTTG	AGATAŤTGAA	360
GGTGCCCAA					•	369

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:191:

TGACACCTTG	TCCAGCATCT	GCACAGGGAA	AAGAAACTAT	TATCAGAGTG	AÁCAGGCAAC	60
CTACAGAATG	GGAGAAAATT	TTTGCAATCT	ATCCATCTGA	CAAAGGGCTA	ATATCCAGAA	120
TCTACAAAGA	ACTTATACAA	ATTTACAAGA	AACAAACAAA	CAAACAACTC	CTCAAAAAGT	180
GGGTGAAGGA	TGTGAACAGA	CACTTCTCAA	AAGAAGACAT	TTATGGGGCC	AACAAACATA	240
TGAAAAAAG	CTCATCATCA	CTGGTCACTA	GATAAATGCA	AATCAAAACC	ACAATGAGAT	300
ACCATCTCAT	TCCAGTTAGA	ATGGCAATCA	TTAAAAAGTC	AGGAAACAAC	AGATGCTGGA	360
CAAGGTGTC						369

(2) INFORMATION FOR SEQ ID NO:192: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 449 base pairs

- - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGACGCTTGG	CCACTTGACA	CTTCATCTTT	GCACAGAAAA	ACTTCTTTAC	AGATTTAATT	60
CAAGACTGGT	CTAGTGACAG	TCCTCCAGAC	ATTTTTTCAT	TTGTTCCATA	TACGTGGAAT	120
TTTAAAATCA	TGTTTCATCA	GTTTGAAATG	ATTTGGGCTG	CTAATCAACA	CAATTGGATC	180
GACTGTTCTA	CTAAACAACA	GGAAAATGTG	TATCTGGCAG	CCTGTGGAGA	AACACTAAAC	240
ATTGATTTTT	CTTTGCCTTT	TACGGACTTT	GTTCCAGCTA	CATGTAATAC	CAAGTTCTCT	300
TTAAGAGGAG	AAGATGTTGA	TCTTCATTTG	TTTCTACCAG	ACTGCCACCC	TAGTAAATAT	360
TCTTTATTTA	TGCTGGTAAA	AAATTGCCAT	CCAAATAAGA	TGATTCATGA	TACTGGTATT	420
CCTGCTGAGT	GTCAAGTGGC	CAAGCGTCA				449

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGACGCTTGG	CCACTTGACA	CCAGGGATGT	AKCAGTTGAA	TATAATCCTG	CAATTGTACA	60
TATTGGCAAT	TTCCCATCAA	ACATTCTAGA	AAGAGACAAC	CAGGATTGCT	AGGCCATAAA	120
AGCTGCAATA	AATAACTGGT	AATTGCAGTA	ATCATTTCAG	GCCAATTCAA	TCCAGTTTGG	180
CTCAGAGGTG	CCTTTGGCTG	AGAGAAGAGG	TGAGATATAA	TGTGTTTTCT	TGCAACTTCT	240
TGGAAGAATA	ACTCCACAAT	AGTCTGAGGA	CTAGATACAA	ACCTATTTGC	CATTAAAGCA	300
CCAGAGTCTG	TTAATTCCAG	TACTGATAAG	TGTTGGAGAT	TAGACTCCAG	TGTGTCAAGT	360
GGCCAAGCGT	CA					372

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGACGCTTGG	CCACTTGACA	CTTATGTAGA	ATCCATCGTG	GGCTGATGCA	AGCCCTTTAT	60
TTAGGCTTAG	TGTTGTGGGC	ACCTTCAATA	TCACACTAGA	GACAAACGCC	ACAAGATCTG	120
CAGAAACATT	CAGTTCTGAN	CACTCGAATG	GCAGGATAAC	TTTTTGTGTT	GTAATCCTTC	180
ACATATACAA	AAACAAACTC	TGCANTCTCA	CCTTACAAAA	AAACGTACTG	CTGTAAAATA	240
TTAAGAAGGG	GTAAAGGATA	CCATCTATAA	CAAAGTAACT	TACAACTAGT	GTCAAGTGGC	300
CAAGCGTCA						309

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH: 312 base pairs
(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: single
(D)	TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TGACGCTTGG	CCACTTGACA	CCCAATCTCG	CACTTCATCC	TCCCAGCACC	TGATGAAGTA	60
GGACTGCAAC	TATCCCCACT	TCCCAGATGA	GGGGACCAAN	GTACACATTA	GGACCCGGAT	120
GGGAGCACAG	ATTTGTCCGA	TCCCAGACTC	CAAGCACTCA	GCGTCACTCC	AGGACAGCGG	180
CTTTCAGATA	AGGTCACAAA	CATGAATGGC	TCCGACAACC	GGAGTCAGTC	CGTGCTGAGT	240
TAAGGCAATG	GTGACACGGA	TGCACGTGTN	ACCTGTAATG	GTTCATCGTA	AGTGTCAAGT	300
GGCCAAGCGT	CA			• .		312

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TGTATCGACG TAGTGGT	CTC CTCAGCCATG	CAGAACTGTG	ACTCAATTAA	ACCTCTTTCC	60
TTTATGAATT ACCCAAT	CTC GGGTAGTGTC	TTTATAGTAG	TGTGAGAATG	GACTAATACA	120
AGTACATTTT ACTTAGT	AAT AATAATAAAC	AAATATATTA	CATTTTTGTG	TATTTACTAC	180
ACCATATTTT TTATTGTT	TAT TGTAGTGTAC	ACCTTCTACT	TATTAAAAGA	AATAGGCCCG	240
AGGCGGGCAG ATCACCAC	GGT CAGGAGATGG	AGACCACTAC	GTCGATAC	•	288
		4			

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTGGGCACCT	TCAATATCAT	GACAGGTGAT	GTGATAACCA	AGAAGGCTAC	TAAGTGATTA	60
ATGGGTGGGT	AATGTATACA	GAGTAGGTAC	ACTGGACAGA	GGGGTAATTC	ATAGCCAAGG	120
CAGGAGAAGC	AGAATGGCAA	AACATTTCAT	CACACTACTC	AGGATAGCAT	GCAGTTTAAA	180
ACCTATAAGT	AGTTTATTTT	TGGAATTTTC	CACTTAATAT	TTTCAGACTG	CAGGTAACTA	240
AACTGTGGAA	CACAAGAACA	TAGATAAGGG	GAGACCACTA	CGTCGATAC		289
	***	*				

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GTATCGACGT	AGTGGTCTCC	CAAGCAGTGG	GAAGAAAACG	TGAACCAATT	AAAATGTATC	60
AGATACCCCA	AAGAAAGGCG	CTTGAGTAAA	GATTCCAAGT	GGGTCACAAT	CTCAGATCTT	120
AAAATTCAGG	CTGTCAAAGA	GATTTGCTAT	GAGGTTGCTC	TCAATGACTT	CAGGCACAGT	180
CGGCAGGAGA	TTGAAGCCCT	GGCCATTGTC	AAGATGAAGG	AGCTTTGTGC	CATGTATGGC	240
AAGAAAGACC	CCAATGAGCG	GGACTCCTGG	AGACCACTAC	GTCGATAC		288

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTTTTTGGG	AAAAACNCAA	NTGGGGGAAA	GGGGGNTTNN	TNGCAAGGGG	ATAAAGGGGG	60
AANCCCAGGG	TTTCCCCATT	CAGGGAGGTG	TAAAAAGNCG	GCCAGGGGAT	TGTAANAGGA	120
TTCAATAATA	GGCGGAATGG	GCCCNGAAGT	TGCAAGGTTC	CNGCCCGCCA	TGNCCGCGGG	180
ATTTAGTGAC	ATTACGACGS	TGGTAATAAA	GTGGGSCCAA	WAAATATTTG	TGATGTGATT	240
TTTSGACCAG	TGAACCCATT	GWACAGGACC	TCATTTCCTY	TGAGATGRTA	GCCATAATCA	300
GATAAAAGRT	TAGAAGTYTT	TCTGCACGTT	AACAGCATCA	TTAAATGGAG	TGGCATCACC	360
AATTTCACCC	TTTGTTAGCC	GATACCTTCC	CCTTGAAGGC	ATTCAATTAA	GTGACCAATC	420
GTCATACGAG	AGGGGATGGC	ATGGGGATTG	ATGATGATAT	CAGGGGTGAT	ACCTTCACAG	480
GTGAAAGGCA	TATCCTCTTG	TCTATACTGA	ATACCACAAG	TACCCTTTTG	ACCATGTCGA	540
CTAGCAAATT	TGTCTCCAAT	CTGTGTWATC	CCTAACAGAG	CGTACCCTTA	TTTTACAAAA	600
TTTATATCCT	TCCTGATTGA	GAGTTACCAT	AACCTGATCC	ACAATGCCCG	TCTCGCTWGT	660
TCTGAGAAAA	GTGCTACAGT	CTCTCTTGGT	ATAGCGTCTA	TTGGTGCTCT	CCAATTCATC	720
TTCATTTTTC	AGGCAAGGTG	AACTGTTTTG	CCTATAATAA	CMTCATCTCC	TGATACMCGA	780
AACCCCKGGA	RCTATCAAAC	CATCATCATC	CAGCGTTCKT	WATGTYMCTA	AATCCCTATT	840
GCGGCCGCCT	GCAGGTCAAC	ATATNGGAAA	ACCCCCCACC	CCTTNGGAGC	NTACCTTGAA	900
TTTTCCATAT	GTCCCNTAAA	TTANCTNGNC	TTANCCTGGC	CNTAACCTNT	TCCGGTTTAA	960
ATTGTTTCCG	CCCCCNTTCC	CCNCCTTNNA	ACCGGAAACC	TTAATTTTNA	ACCNGGGGTT	1020
CCTATCC						1027

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

AGTGACATTA	CGACGCTGGC	CATCTTGAAT	CCTAGGGCAT	GAAGTTGCCC	CAAAGTTCAG	60
CACTTGGTTA	AGCCTGATCC	CTCTGGTTTA	TCACAAAGAA	TAGGATGGGA	TAAAGAAAGT	120
GGACACTTAA	ATAAGCTATA	AATTATATGG	TCCTTGTCTA	GCAGGAGACA	ACTGCACAGG	180

TATACTACCA GCGTCGTAAT GTCACTA	
(2) INFORMATION FOR SEQ ID NO:201:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
TGGGCACCTT CAATATCTAT TAAAAGCACA AATACTGAAG AACACCCAA GACTATCAAT GAGGTTACAT CTGGAGTCCT CGATATATCA GGAAAAAATG AAGTGAACAT TCACAGAGTT TTACTTCTTT GGGAACTCAA ATGCTAGAAA AGAAAAGGGT GCCCTCTTTC TCTGGCTTCC TGGTCCTATC CAGCGTCGTA ATGTCACTA	
(2) INFORMATION FOR SEQ ID NO:202:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202: 	
NTACGCTGCA ACACTGTGGA GCCACTGGTT TTTATTCCCG GCAGGTTATC CAGCAAACAG TCACTGAACA CACCGAAGAC CGTGGTATGG TAACCGTTCA CAGTAATCGT TCCAGTCGTC TGCGGGACCC CGACGAGCGT CACTGGGTAC AGACCAGATT CAGCCGGAAG AGAAAGCGCC GCAGGGAGAG ACTCGAACTC CACTCCGCTG GTGAGCAGCC CCATGTTTTC AACTCGAAGT TCAAACGGCA TTGGGTTATA TACCATCAGC TGAACTTCAC ACACATCTCC TTGAACCCAC TGGAAATCTA TTTTCTTGTT CCGCTCTTCT CCACAGTGTT GCAGCGTAA	
(2) INFORMATION FOR SEQ ID NO:203:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:	
TGCTCCTCTT GCCTTACCAA CCCAAAGCCC ACTGTGAAAT ATGAAGTGAA TGACAAAATT CAGTTTTCAA CGCAATATAG TATAGTTTAT CTGATTCTTT TGATCTCCAG GACACTTTAA ACAACTGCTA CCACCACCAC CAACCTAGGG ATTTAGGATT CTCCACAGAC CAGAAATTAT TTCTCCTTTG AGTTTCAGGC TCCTCTGGGA CTCCTGTTCA TCAATGGGTG GTAAATGGCT A	
(2) INFORMATION FOR SEQ ID NO:204:	

(QUENCE CHAR A) LENGTH: B) TYPE: nu C) STRANDED D) TOPOLOGY	248 base pacted acid	airs		
(xi) SE	QUENCE DESC	CRIPTION: S	EQ ID NO:20	4:	
					GGCGATTTGA
					CAAAAATTCA
					TAATGTTTCA TGGTAAGGCA
AGAGGAGC		AGAGATGATT	recharano	AMOCCOTOT	IGGIAAGGCA
_					
(2) INFORMA	TION FOR SE	Q ID NO:20	5 :		
(i) SE	QUENCE CHAR	ACTERISTIC	S:		
	A) LENGTH:				
	B) TYPE: nu				
	C) STRANDEDD) TOPOLOGY	_	ıe		
· ·	D, TOPOLOGI	. IIncar			
(xi) SE	QUENCE DESC	CRIPTION: S	EQ ID NO:20	5:	
TACGCTGCAA	CACTGTGGAG	CCATTCATAC	AGGTCCCTAA	TTAAGGAACA	AGTGATTATG
CTACCTTTGC	ACGGTTAGGG	TACCGCGGCC	GTTAAACATG	TGTCACTGGG	CAGGCGGTGC
				CAGGCGGGGT	
				CCTGTGTTGG	
					CAGTTCAGTG
					TACTAACATT TTATATGTTT
				TTAATTGGTG	
	GGGTGGTAAA		Granddellife	11111110010	GCTGCTTTTM
(2) INFORMA	ATION FOR SE	EQ ID NO:20	6:		
(i) SI	QUENCE CHAR) ス <i>C</i> T'ED T CTT C	c.		
	(A) LENGTH:				
	B) TYPE: nu	-			
	(C) STRANDED				
	D; TOPOLOGY	_			
(xi) SE	QUENCE DESC	CRIPTION: S	EQ ID NO:20	6 :	
ፕ ልርልርፕርአርፕ	CATGTCCCCT	ACCADAGCCC	ATGTAAGGAG	CTGAGTTCTT	AAAGACTGAA
INDICIONCI		TICCERTICCE.			TATACACTOM

GGCCGGGCAT GGTAGCACAC ACCTGTAATC CCAGCTACTA GGGGACATGA GTCAGTCTA 179

- (2) INFORMATION FOR SEQ ID NO:207:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 base pairs

(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:	
AGACTGACTC ATGTCCCCTA CCCCACCTTC TGCTGTGCTG	
(2) INFORMATION FOR SEQ ID NO:208:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:	
AGACTGACTC ATGTCCCCTA TTTAACAGGG TCTCTAGTGC TGTGAAAAAA AAAAATGCTG AACATTGCAT ATAACTTATA TTGTAAGAAA TACTGTACAA TGACTTTATT GCATCTGGGT AGCTGTAAGG CATGAAGGAT GCCAAGAAGT TTAAGGAATA TGGGTGGTAA ATGGCTAGGG GACATGAGTC AGTCTA	60 120 180 196
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 345 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:	
GACGCTTGGC CACTTGACAC CTTTTATTT TTAAGGATTC TTAAGTCATT TANGTNACTT TGTAAGTTTT TCCTGTGCCC CCATAAGAAT GATAGCTTTA AAAATTATGC TGGGGTAGCA AAGAAGATAC TTCTAGCTTT AGAATGTGTA GGTATAGCCA GGATTCTTGT GAGGAGGGGT GATTTAGAGC AAATTTCTTA TTCTCCTTGC CTCATCTGTA ACATGGGGAT AATAATAGAA CTGGCTTGAC AAGGTTGGAA TTAGTATTAC ATGGTAAATA CATGTAAAAT GTTTAGAATG GTGCCAAGTA TCTAGGAAGT ACTTGGGCAT GGGTGGTAAA TGGCT (2) INFORMATION FOR SEQ ID NO:210:	60 120 180 240 300 345
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GACGCTTGGC	CACTTGACAC	TAGAGTAGGG	TTTGGCCAAC	TTTTTCTATA	AAGGACCAGA	60
GAGTAAATAT	TTCAGGCTTT	GTGGGTTGTG	CAGTCTCTCT	TGCAACTACT	CAGCTCTGCC	120
ATTGTAGCAT	AGAAATCAGC	CATAGACAGG	ACAGAAATGA	ATGGGTGGTA	AATGGCTA	178

- (2) INFORMATION FOR SEQ ID NO:211:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGGGCACCTT	CAATATCTAT	CCAGCGCATC	TAAATTCGCT	TTTTTCTTGA	TTAAAAATTT	60
CACCACTTGC	TGTTTTTGCT	CATGTATACC	AAGTAGCAGT	GGTGTGAGGC	CATGCTTGTT	120
TTTTGATTCG	ATATCAGCAC	CGTATAAGAG	CAGTGCTTTG	GCCATTAATT	TATCTTCATT	180
GTAGACAGCA	TAGTGTAGAG	TGGTATCTCC	ATACTCATCT	${\tt GGAATATTTG}$	GATCAGTGCC	240
ATGTTCCAGC	AACATTAACG	CACATTCATC	TTCCTGGCAT	TGTACGGCCT	TTGTCAGAGC	300
TGTCCTCTTT	TTGTTGTCAA	GGACATTAAG	TTGACATCGT	CTGTCCAGCA	CGAGTTTTAC	360
TACTTCTGAA	TTCCCATTGG	CAGAGGCCAG	ATGTAGAGCA	GTCCTCTTTT	GCTTGTCCCT	420
CTTGTTCACA	TCAGTGTCCC	TGAGCATAAC	GGAA			454

- (2) INFORMATION FOR SEQ 1D NO:212:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCCGTTATGC	CACCCAGAAA	ACCTACTGGA	GTTACTTATT	AACATCAAGG	CTGGAACCTA	60
TTTGCCTCAG	TCCTATCTGA	TTCATGAGCA	CATGGTTATT	ACTGATCGCA	TTGAAAACAT	120
TGATCACCTG	GGTTTCTTTA	TTTATCGACT	GTGTCATGAC	AAGGAAACTT	ACAAACTGCA	180
ACGCAGAGAA	ACTATTAAAG	GTATTCAGAA	ACGTGAAGCC	AGCAATTGTT	TCGCAATTCG	240
GCATTTTGAA	AACAAATTTG	CCGTGGAAAC	TTTAATTTGT	TCTTGAACAG	TCAAGAAAAA	300
CATTATTGAG	GAAAATTAAT	ATCACAGCAT	AACGGAA			337

- (2) INFORMATION FOR SEQ ID NO:213:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 715 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TCGGGTGATG CCTCCTCAGG CATCTTCCAT CCATCTCTTC AAGATTAGCT GTCCCAAATG

TTTTTCCTTC	TCTTCTTTAC	TGATAAATTT	GGACTCCTTC	TTGACACTGA	TGACAGCTTT	120
AGTATCCTTC	TTGTCACCTT	GCAGACTTTA	AACATAAAAA	TACTCATTGG	TTTTAAAAGG	180
			GGCCTTGAAA			240
ATGTCGGTTA	GCTGAACAGA	ATTCATTTTA	CAATGCAGAG	TGAGAAAAGA	AGGGAGCTAT	300
ATGCATTTGA	GAATGCAAGC	ATTGTCAAAT	AAACATTTTA	AATGCTTTCT	TAAAGTGAGC	360
ACATACAGAA	ATACATTAAG	ATATTAGAAA	GTGTTTTTGC	TTGTGTACTA	CTAATTAGGG	420
AAGCACCTTG	TATAGTTCCT	CTTCTAAAAT	TGAAGTAGAT	TTTAAAAACC	CATGTAATTT	480
AATTGAGCTC	TCAGTTCAGA	TTTTAGGAGA	ATTTTAACAG	GGATTTGGTT	TTGTCTAAAT	540
			TTTTATAAAT			600
TTTTCATGCT	GCTATGAAAG	AAATACCCAN	GACAGGGTTA	TTTATAAANG	GAAAGANGTT	660
AATTTGACTC	CCAGTTCACA	GGCCTGAGGA	NGNATCNCCC	GAAATCCTTA	TTGCG	715

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NQ:214:

CCTAANCNCC	ATA CNITCCCT	COMOCOCOCO	acada amaga	agas mindaga		
					TGATGCCTCC	60
					CCATTCCTTC	120
TCCCACCTGC	CTGATTCTTC	ATATGTTGGG	TGTCCCTGTT	TTTCTGGTGC	TATTTCCTGA	180
CTGCTGTTCA	GCTGCCACTG	TCCTGCAAAG	CCTGCCTTTT	TAAATGCCTC	ACCATTCCTT	240
CATTTGTTTC	TTAAATATGG	GAAGTGAAAG	TGCCACCTGA	GGCCGGGCAC	AGTGGCTCAC	300
GCCTGTAATC	CCAGCACTTT	GGGAGCCTGA	GGAGGCATCA	CCCGA		345

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single (D) TCPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGTGATGCCT	CCTCAGGCGA	AGCTCAGGGA	GGACAGAAAC	CTCCCGTGGA	GCAGAAGGGC	60
AAAAGCTCGC	TTGATCTTGA	TTTTCAGTAC	GAATACAGAC	CGTGAAAGCG	GGGCCTCACG	120
ATCCTTCTGA	CCTTTTGGGT	TTTAAGCAGG	AGGTGTCAGA	AAAGTTACCA	CAGGGATAAC	180
			CGTCGCTTTT			240
TTCCTATCAT	TGTGAAGCAG	AATTCACCAA	GCGTTGGATT	GTTCACCCAC	TAATAGGGAA	300
			GGTTAGTTTT			360
TTGCCATGGT	AATCCTGCTC	AGTACGAGAG	GAACCGCAGG.	TTCASACATT	TGGTGTATGT	420
GCTTGCCTT			•. •			429

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGACACCTAT	GTCCNGCATC	TGTTCACAGT	TTCCACAAAT	AGCCAGCCTT	TGGCCACCTC	60
TCTGTCCTGA	GGTATACAAG	TATATCAGGA	GGTGTATACC	TTCTCTTCTC	TTCCCCACCA	120
AAGAGAACAT	GCAGGCTCTG	GAAGCTGTCT	TAGGAGCCTT	TGGGCTCAGA	ATTTCAGAGT	180
CTTGGGTACC	TTGGATGTGG	TCTGGAAGGA	GAAACATTGG	CTCTGGATAA	GGAGTACAGC	240
CGGAGGAGGG	TCACAGAGCC	CTCAGCTCAA	CCCCCTGTGC	CTTAGTCTAA	AAGCAGCTTT	300
GGATGAGGAA	GCAGGTTAAG	TAACATACGT	AAGCGTACAC	AGGTAGAAAG	TGCTGGGAGT	360
CAGAATTGCA	CAGTGTGTAG	GAGTAGTACC	TCAATCAATG	AGGGCAAATC	AACT'GAAAGA	420
AGAAGACCNA	TTAATGAATT	GCTTANGGGG	AAGGATCAAG	GCTATCATGG	AGATCTTTCT	480
AGGAAGATTA	'ITG'I'I'TANAA	TTATGAAAGG	ANTAGGGCAG	GGACAGGGCC	AGAAGTANAA	540
GANAACATTG	CCTATANCCC	TTGTCTTGCA	CCCAGATGCT	GGACAAGGTG	TCA	593

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TGACACCTTG TCCAGCATO	CT GACGTGAAGA	TGAGCAGCTC	AGAGGAGGTG	TCCTGGATTT	60
CCTGGTTCTG TGGGCTCCC	ET GGCAATGAAT	TCTTCTGTCA	AGTGGATGAA	GACTACATCC	120
AGGACAAATT TAATCTTAG	T GGACTCAATG	AGCAGGTCCC	TCACTATCGA	CAAGCTCTAG	180
ACATGATCTT GGACCTGGA	AG CCTGATGAAG	AACTGGAAGA	CAACCCCAAC	CAGAGTGACC	240
TGATTGAGCA GGCAGCCGA	AG ATGCTTTATG	GATTGATCCA	CGCCCGCTAC	ATCCTTACCA	300
ACCGTGGCAT CGCCCAGA	rg crggacaagg	TGTCA			335

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TACGTACTGG	TCTTGAAGGT	CTTAGGTAGA	GAAAAAATGT	GAATATTTAA	TCAAAGACTA	60
TGTATGAAAT	GGGACTGTAA	GTACAGAGGG	AAGGGTGGCC	CTTATCGCCA	GAAGTTGGTA	120
GATGCGTCCC	CGTCATGAAA	TGTTGTGTCA	CTGCCCGACA	TTTGCCGAAT	TACTGAAATT	180
CCGTAGAATT	AGTGCAAATT	CTAACGTTGT	TCATCTAAGA	TTATGGTTCC	ATGTTTCTAG	240
TACTTTTA						248

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pai	i:	rs
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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGACGCTTGG	CCACTTGACA	CAAGTAGGGG	ATAAGGACAA	AGACCCATNA	GGTGGCCTGT	60
CAGCCTTTTG	TTACTGTTGC	TTCCCTGTCA	CCACGGCCCC	CTCTGTAGGG	GTGTGCTGTG	120
CTCTGTGGAC	ATTGGTGCAT	TTTCACACAT	ACCATTCTCT	TTCTGCTTCA	CAGCAGTCCT	180
GAGGCGGGAG	CACACAGGAC	TACCTTGTCA	GATGANGATA	ATGATGTCTG	GCCAACTCAC	240
CCCCCAACCT	TCTCACTAGT	TATANGAAGA	GCCANGCCTA	NAACCTTCTA	TCCTGNCCCC	300
TTGCCCTATG	ACCTCATCCC	TGTTCCATGC	CCTATTCTGA	TTTCTGGTGA	ACTTTGGAGC	360
AGCCTGGTTT	NTCCTCCTCA	CTCCAGCCTC	TCTCCATACC	ATGGTANGGG	GGTGCTGTTC	420
CACNCAAANG	GTCAGGTGTG	TCTGGGGAAT	CCTNANANCT	GCCNGGAGTT	TCCNANGCAT	480
TCTTAAAAAC	CTTCTTGCCT	AATCANATNG	TGTCCAGTGG	CCAACCNTCN		530

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(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGACGCTTGG	CCACTTGACA	CTAAATAGCA	TCTTCTAAAG	GCCTGATTCA	GAGTTGTGGA	60
				TCCTGTGCTC		120
CTGTGTTTCT	GCTGGAAAAG	GAGGGAAGAG	GAATGGCTGA	TTTTTACCTA	ATGTCTCCCA	180
GTTTTTCATA	TTCTTCTTGG	ATCCTCTTCT	CTGACAACTG	TTCCCTTTTG	GTCTTCTTCT	240
TCTTGCTCAG	AGAGCAGGTC	TCTTTAAAAC	TGAGAAGGGA	GAATGAGCAA	ATGATTAAAG	300
AAAACACACT	TCTGAGGCCC	AGAGATCAAA	TATTAGGTAA	ATACTAAACC	GCTTGCCTGC	360
TGTGGTCACT	TTTCTCCTCT	TTCACATGCT	CTATCCCTCT	ATCCCCCACC	TATTCATATG	420
GCTTTTATCT	GCCAAGTTAT	CCGGCCTCTC	ATCAACCTTC	TCCCCTAGCC	TACTGGGGGA	480
TATCCATCTG	GGTCTGTCTC	TGGTGTATTG	GTGTCAAGTG	GCCAAGCGTC	A	531

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

				- .		
ATTGACGCTT	GGCCACTTGA	CACCCGCCTG	CCTGCAATAC	TGGGGCAAGG	GCCTTCACTG	60
CTTTCCTGCC	ACCAGCTGCC	ACTGCACACA	GAGATCAGAA	ATGCTACCAA	CCAAGACTGT	120
TGGTCCTCAG	CCTCTCTGAG	GAGAAAGAGC	AGAAGCCTGG	AAGTCAGAAG	AGAAGCTAGA	180
TCGGCTACGG	CCTTGGCAGC	CAGCTTCCCC	ACCTGTGGCA	ATAAAGTCGT	GCATGGCTTA	240
ACAATGGGGG	CACCTCCTGA	GAAACACATT	GTTAGGCAAT	TCGGCGTGTG	TTCATCAGAG	300

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CATATTTACA	CAAACCTCGA	TAGTGCAGCC	TACTATCCAC	TATTGCTCCT	ACGCTGCAAA	360
CCTGAACAGC	ATGGGACTGT	ACTGAATACT	GGAAGCAGCT	GGTGATGGTA	CTTATTTGTG	420
TATCTAAACA	CAGAGAAGGT	ACAGTAAGAA	TATGGTATCA	TAAACTTACA	GGGACCGCCA	480
TCCTATATGC	AGTCTGTTGT	GACCAAAATG	TGTCAAGTGG	CCAAGCGTCA		530

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTATCGACG	TAGTGGTCTC	CGGGCTACTA	GGCCGTTGTG	TGCTGGTAGT	ACCTGGTTCA	60
CTGAAAGGCG	CATCTCCCTC	CCCGCGTCGC	CCTGAAGCAG	GGGGAGGACT	TCGCCCAGCC	120
AAGGCAGTTG	TATGAGTTTT	AGCTGCGGCA	CTTCGAGACC	TCTGAGCCCA	CCTCCTTCAG	180
GAGCCTTCCC	CGATTAAGGA	AGCCAGGGTA	AGGATTCCTT	CCTCCCCAG	ACACCACGAA	240
CAAACCACCA	CCCCCCCTAT	TCTCGCACCC	CATATACATC	AGAACGAAAC	AAAAATAA.CA	300
AATAAACNAA	AACCAAAAAA	AAAAGAGAAG	GGGAAATGTA	TATGTCTGTC	CATCCTGTTG	360
CTTTAGCCTG	TCACCTCCTA	NAGGGCAGGC	ACCGTGTCTT	CCGAATGGTC	TGTGCAGCGC	420
CGACTGCGGG	AAGTATCGGA	CCAGGAAGCA	GAGTCAGCAG	AAGTTGAACG	GTGGGCCCGG	480
CGGCTCTTGG	GGGCTGGTGT	TGTACTTCGA	GACCGCTTTC	GCTTTTTGTC	TTAGATTTAC	540
GTTTGCTCTT	TGGAGTCGCA	NACCACTACN	TCNATACA			578

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGTATCGACG	TAGTGGTCTC	CTCTTGCAAA	GGACTGGCTG	GTGAATGGTT	TCCCTGAATT	60
ATGGACTŢAC	CCTAAACATA	TCTTATCATC	ATTACCAGTT	GCAAAATATT	AGAATCTGTT	120
GTCACTGTTT	CATTTGATTC	CTAGAAGGTT	AGTCTTAGAT	ATGTTACTTT	AACCTGTATG	180
CTGTAGTGCT	TTGAATGCAT	TTTTTGTTTG	CATTTTTGTT	TGCCCAACCT	GTCAATTATA	240
GCTGCTTAGG	TCTGGACTGT	CCTGGATAAA	GCTGTTAAAA	TATTCACCAG	TCCAGCCATC	300
TTACAAGCTA	ATTAAGTCAA	CTAAATGCTT	CCTTGTTTTG	CCAGACTTGT	TATGTCAATC	360
CTCAATTTCT	${\tt GGGTTCATTT}$	TGGGTGCCCT	AAATCTTAGG	GTGTGACTTT	CTTAGCATCC	420
TGTAACATCC	ATTCCCAAGC	AAGCACAACT	TCACATAATA	CTTTCCAGAA	GTTCATTGCT	480
GAAGCCTTTC	CTTCACCCAG	CGGAGCAACT	TGATTTTCTA	CAACTTCCCT	CATCAGAGCC	540
ACAAGAGTAT	GGGATATGGA	GACCACTACG	TCGATACA			578

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ΙD	NO:2	24	:
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TGTATCGACG	TANTGGTCTC	CCAAGGTGCT	GGGATTGCAG	GCATGAGCCA	CCACTCCCAG	60
GTGGATCTTT	TTCTTTATAC	TTACTTCATT	AGGTTTCTGT	TATTCAAGAA	GTGTAGTGGT	120
AAAAGTCTTT	TCAATCTACA	TGGTTAAATA	ATGATAGCCT	GGGAAATAAA	TAGAAATTTT	180
TTCTTTCATC	TTTAGGTTGA	ATAAAGAAAC	AGAAAAAATA	GAACATACTG	AAAATAATCT	240
AAGTTCCAAC	CATAGAAGAA	CTGCAGAAGA	AATGAAGAAA	GTGATGATGA	TTTAGATTTT	300
GATATTGATT	TAGAAGACAC	AGGAGGAGAC	CACTACGTCG	ATACA		345

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TGTATCGACG TAGTGGTCTC CAAACTGAGG TATGTGTGCC ACTAGCACAC AAAGCCTTCC 60
AACAGGGACG CAGGTATAAAG GGAATCTGTT TCTAAATTAA TTTCCACCTT 120
CTCTAAGTAT TCTTTCCTAA AACTGATCAA GGTGTGAAGC CTGTGCTCTT TCCCAACTCC 180
CCTTTGACAA CAGCCTTCAA CTAACACAAG AAAAGGCATG TCTGACACTC TTCCTGAGTC 240
TGACTCTGAT ACGTTGTTCT GATGTCTAAA GAGCTCCAGA ACACCAAAGG GACAATTCAC 300
AATGCTGGTG TATAACAGAC TCCAATGGAG ACCACTACGT CGATACA 347

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

AGGNGNGGGA	NTGTATCGAC	GTAGTGGTCT	CCCAACAGTC	TGTCATTCAG	TCTGCAGGTG	60
				CTCCTCAGCT		120
AAATTAAATĊ	TTGTCATGAC	AAGTCTGGAA	TTCCTGATGA	GGTTTTACAA	AGTATTTTGG	180
ATCAATACTC	CAACAAATCA	GAAAGCCAGA	AAGAGGATCC	TTTCAATATT	GCAGAACCAC	240
GAGTGGATTT	ACACACCTCA	GGAGACCACT	ACGTCGATAC	A		281

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGGAAACACT	TCCTCCCAGC	CTTGTAAGGG	TTGGAGCCCT	CTCCAGTATA	TGCTGCAGAA	60
TTTTTCTCTC	GGTTTCTCAG	AGGATTATGG	AGTCCGCCTT	AAAAAAGGCA	AGCTCTGGAC	120
ACTCTGCAAA	GTAGAATGGC	CAAAGTTTGG	AGTTGAGTGG	CCCCTTGAAG	GGTCACTGAA	180

	GTTCAAGCTG					240
	ATTGATCAAT				TGGCTCCACT	3 0 0
	TCATAATTTT		TCCTCCTGAG	_	TTTTCGCCTC	360
	CGGTTCGGCT			TGAAGAAGAG		420
				AGGGTCATCC	CATGTCTCCT	480
		TCATCACCCA			TGGTGGGAGG	540
	TCTACTACCA				GAGTGCTCCA	600
	GGTTTATGTC					660
	TOTOTGAAAA			TGATGGAGTC	TGTACTCTGG	720
	CCACCTGGGA			TGACCCTTTT	CACCTCTGAA	780
	GTATCCAAAG			TCACATCAAC		840
GAGGAGGAAG	CTAGAGGAAT	AGTGATTAGA			GGGACCCAAA	900
TTTCTCAAGT	GGAGGGAGAA				TGGGTATTCA	960
GGGAGCTGCT	CAGAAACCTA	TAAACTTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	1020
TGAGTCACCA	GCAGTGTTTT	TAGAGCACCT	CCAGGAGGCT	TATCAGATTT	ACACCCCTTT	1080
TGACCTGGCA	GCCCCGAAA	ATAGCCATGC	TCTTAATTTG	GCATTTGTGG	CTCAGGCAGC	1140
CCCAGATAGT	AAAAGGAAAC	TCCAAAAACT	AGAGGGATTT	TGCTGGAATG	AATACCAGTC	1200
AGCTTTTAGA	GATAGCCTAA	AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAAACAAG	1260
CAGCTCAGGC	AGCTGAAAAA	AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	1320
TAGATCAGCC	TCATTTGACT	TCCCCTCCCA	CATGGTGTTT	AAATCCAGCT	ACACTACTTC	1380
CTGACTCAAA	CTCCACTATT	CCTGTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	1440
CTGGCCGACC	TGATCTTCAA	AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	ATGTTCACAG	1500
ACAGTAGCAG	CTTCCTCGAG	AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	1560
CAGATGTGTT	GTGGGCTCAG	GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	1620
TCGCCCTCAC	TCAGGCTCTC	CGATGGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	1680
ACGCCTTTGC	TRITGTGCAT	GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	1740
CAGCAGGTGG	CTGTAATCCA	CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCGT	1800
GGTAACCAGA	AAGCTGATTC	AGCACCTCAA	GATGCAGTGT	GACTTTCAGT	CACGCCTCTA	1860
AACTTGCTGC	CCACAGTCTC	CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	1920
ACAGAAGAAG	AAAACTGGCC	TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	1980
TTCTTCCTGA	CTCTAGAATC	TTCATACCCC	GAACTCTTGG	GAAAACTTTA	ATCAGTCACC	2040
TACAGTCTAC	CACCCATTTA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	2100
AGATCCCCCA	TUTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	2160
AGGTAAATGC	CAAAAAAGGT	CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	2220
CAGGAGAAAA	GTGGGAAATT	GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	2280
ACCTTCTAGT				AGCATTTGCT		2340
AAACTGTCAA	TATGGTAGTT	AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CATGGGCTGC	2400
	TAGGGTCTGA				TTAGTCAGTC	2460
AGTAAGGCGT	TAAACATTCA	ATGGAAGCTC	CATTGTGCCT	ATCGACCCCA	GAGCTCTGGG	2520
	GCATGAACTG					2580
	GTGTAAGTCT					2640
	TCTTACCTTT					2700
	CCTAATTGGC					2760
	TACAAGATAT					2820
	CAGGGCCCTG					2880
	AAGGACTCCC					2940
	AGGTGGATGG					3000
	AACTAGAAAC					3060
	TGAAGCCATT					3120
	ACTTATGTAT					3180
	ATTCCCCCAA					3240
	TTTAGACTCT					
						3300
	AGCTAAGAGC					3360
	ACTTAACTTG					3420
GATAAGATAC	TGTGGCAAGC	TATATCCGCA	GTTCCCAGGA	ATTCGTCCAA	TIGATCACAG	3480

CCCCTCTACC CTTCAGCAAC CACCACCCTG ATCAGTCAGC GGCCCTCCAC CAGCAAAAAG ATTCTGACTC ACTGAAGACT		3540
TAGCAGTAAA GTTTTTTTT CTTTTTCTTT CTTTTTTTCT		3600 3646
		2040
(2) INFORMATION FOR SEQ ID NO:228:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 419 base pairs	•	
(B) TYPE: nucleic acid	1.	
(C) STRANDEDNESS: single.	: .	
(D) TOPOLOGY: linear		
(· · ·) NOT BOW B BUSH	1.5	
(ii) MOLECULE TYPE: cDNA:	· · · · · · · · · · · · · · · · · · ·	
(vi) ORIGINAL SOURCE:		
- (A) ORGANISM: Homo sapiens	* * * * * * * * * * * * * * * * * * * *	
The same supplies		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22	8:	
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TAAGAGGGTA CAAGATCTAA GCAÇAGCCGT CAATGCAGAA	CACAGAACGT AGCCTGGTAA	60
GTGTGTTAAG AGTGGGAATT TTTGGAGTAC AGAGTAAGGC	ACCTAACCCT AGCTGGGGTT	120
TGGTGACGGT CCCAGATGGC TTACAGAAGA AAGTGTCCTG	AGATGAGTTT TTAAGAATGA	180
ATAAGGATAG ACACAAGTGA GGACTGACTT GGCAGTGGTG		240
TTCGCATGTA TGGAAACTGC ACGTACAGGA ATGAAGAATG	AGACTGTGTG GTGTTTAATG	300
AGCTGCAAAT ACTAATTTTA TCCTGAAAGT TTTGAAGAGT GTAAGGAAAT AACCCTACAT TTCAGGGTTA TTGTTTGTTT	TAACTAAAAA GTATTTTTA	360
		419
(2) INFORMATION FOR SEQ ID NO:229:	7	
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 148 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single	*	
(D) TOPOLOGY: linear		
(11) MOLECULE TYPE: CDNA		
(with CRICIAN) Council		
(vi) CRIGINAL SOURCE:		
(A) ORGANISM: Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22	٥.	
(MI) SEQUENCE DESCRIPTION: SEQ ID NO:22	9: .	
AAGAGGGTAC CTGTATGTAG CCATGGTGGC AATGAGAGAC	TGATTACTAC CTGCTGGAGA	60
TTGTTTAAGT GAGTTAATAT ATTAAGGATA AAGGCAGCCA		120
AGGAAATTAC AGATATTGAA GGTCCCAA		148
one is well as a second of	*	
(2) INFORMATION FOR SEQ ID NO:230:	·	
(i) SEQUENCE CHARACTERISTICS:	. C	
(A) LENGTH: 257 base pairs	• • • •	
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear	• • • • • • • • • • • • • • • • • • • •	
(ii) MOLECULE TYPE: cDNA		

<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo Sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:	
TAAGAGGGTA CMAAAAAAA AAAATAGAAC GAATGAGTAA GACCTACTAT TTGATAGTAC AACAGGGTGA CTATAGTCAA TGATAACTTA ATTATACATT TAACATAGAG TGTAATTGGA CTGTTTGTAA CTCGAAGGAT AAATGCTTGA GAGGATGGAT ACCCCATTCT CCATGATGTA CTTATTTCAC ATTACATGCC TGTATCAAAG CATCTCATAT ACCCTATAAA TATGTACACC TACTATGTAC CCTCTTA	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:231:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:	
TAAGAGGGTA CGGGTATTTG CTGATGGGAT TTTTTTTTT TTCTTTTTTTT TTGGAAAACA AAATGAAAGC CAGAACAAAA TTATTGAACA AAAGACAGGG ACTAAATCTG GAGAAATGAA GTCCCCTCAC CTGACTGCCA TTTCATTCTA TCTGACCTTC CAGTCTAGGT TAGGAGAATA GGGGGTGGAG GGGATTAATC TGATACAGGT ATATTTAAAG CAACTCTGCA TGTGTGCCAG AAGTCCATGG TACCCTCTTA	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:232:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	

TGCTCCTCTT	GCCTTACCAA	CCACAAATTA	GAACCATAAT	GAGATGTCAC	CTCATACCTG	60
GTGGGATTAA	CATTATTTAA	AAAATCAGAA	GTATTGACAA	GGATGTGAAG	AAATTAGAAC	120
ATCTGTGCAC	TGTTGGTGGG	AATGTAAAAA	AGGTGTGGCC	ACTATGGGTA	ACAGCATGAA	180
GGTTCCTCAA	AAAAAATTTT	TTTTAATCTA	CTCTATGATC	GATCTTGAGG	TTGTTTATGC	240
AAAAGAACTG	AAATCAGGAT	TTTGACGAAA	TATTCACATT	CCCACATCCA	TTTCTGCTTT	300
ATTCATAATA	CTCAAGAGAT	GGAAACAACC	TAAATGTCCA	TCCCGGGATG	AATGGATAAA	360
CACAGTGTGG	TATATGCATA	CAATGGAATA	TTATTTAGTC	TTTAAAAAGA	AAAATTCTAT	420

(xi) SEQUENCE DESCRIPTION: SEQ JD NO 232:

CATATACTAC AACTTANATN AACCTTGAGG ACACAATGCT NAGTGAAATA AGCCACGGAA GGACGAATAC TGCATTATTC CCTTATATGA AGTATCTAAA GTGGTCAAAC TCTTANAGCA NAAAGTAAAA ATGGGTGGTT GCCANACAGT TGGTTAGGCN AGAAGANAAN CCTANT	480 540 596
(2) INFORMATION FOR SEQ ID NO:233:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 96 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:	
TCTTCTGAAG ACCTTTCGCG ACTCTTAAGC TCGTGGTTGG TAAGGCAAGA GGAGCGTTGG TAAGGCAAGA GGAGCATGG TAAGGCAAGA GGAGCA	60 96
(2) INFORMATION FOR SEQ ID NO:234:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:	
TGTAAGTCGA GCAGTGTGAT GATAAAACTT GAATGGATCA ATAGTTGCTT CTTATGGATG AGCAAAGAAA GTAGTTCTT GTGATGGAAT CTGCTCCTGG CAAAAATGCT GTGAACGTTG TTGAAAAGAC AACAAAGAGT TTAGAGTAGT ACATAAATTT AGAATAGTAC ATAAACTTAG AATAGTACAT AAACTTAGTA CATAAATAAT GCACGAAGCA GGGGCAGGGC TTGAGAGAAT TGACTTCAAT TTGGAAAGAG TATCTACTGT AGGTTAGATG CTCTCAAACA GCATCACACT GCTCGACTTA CAA	60 120 180 240 300 313
(2) INFORMATION FOR SEQ ID NO:235:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 550 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (vi) ORIGINAL SOURCE:	

121	ODGANTON		
(A)	ORGANISM:	Homo	sablens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AACGAGGACA	GATCCTTAAA	AAGAATGTTG	AGTGAAAAA	GTAGAAAATA	AGATAATCTC	60
CAAAGTCCAG	TAGCATTATT	TAAACATTTT	TAAAAAATAC	ACTGATAAAA	ATTTTGTACA	120
TTTCCCAAAA	ATACATATGG	AAGCACAGCA	GCATGAATGC	CTATGGGRTT	GAGGATAGGG	180
GTTGGGAGTA	GGGATGGGGA	TAAAGGGGGA	AAATAAAACC	AGAGAGGAGT	CTTACACATT	240
TCATGAACCA	AGGAGTATAA	TTATTTCAAC	TATTTGTACC	WGAAGTCCAG	AAAGAGTGGA	300
GGCAGAAGGG	GGAGAAGAGG	GCGAAGAAAC	GTTTTTGGGA	GAGGGGTCCC	ASAAGAGAGA	360
TTTTCGCGAT	GTGGCGCTAC	ATACGTTTTT	CCAGGATCCC	TTAAGCTCTG	CACCCTATTT	420
TTCTCATCAC	TAATATTAGA	TTAAACCCTT	TGAAGACAGC	GTCTGTGGTT	TCTCTACTTC	480
AGCTTTCCCT	CCGTGTCTTG	CACACAGTAG	CTGTTTTACA	AGGGTTGAAC	TGACTGAAGT	540
GAGATTATTC						550

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TAGACTGACT	CATGTCCCCT	ACCAGAGTAG	CTAGAATTAA	TAGCACAAGC	CTCTACACCC	60
AGGAACTCAC	TATTGAATAC	ATAAATGGAA	TTTATTCAGC	CTTAAAAAGT	TTGGAAGGAA	120
ATTCTGACAT	ATGCTAAAAC	ATGGATGAAC	CTTGAAGACT	TTATGATAAG	TAAAAGAAGC	180
CAGTCATAAA	AGGAAAATA	TTGCATGATT	CCACTTATAT	GAGGTACCTA	GAGTAGTCAA	240
TTTCATAGAA	ACACAAAATA	GAATGGTGTT	TGCCAGGGCT	TTTGAGGAAA	AGGGAATGAC	300
AAGTTAGGGG	ACATGAGTCA	GTCTA				325

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TAGACTGACT	CATGTCCCCT	ATCTACTCAA	CATTTCCACT	TGAAGTCTGA	TAGGCATCTC	60
AGACTTATCT	TGTCCCAAAG	CAAACTCTTT	ATTTCTTTTC	ATCCTAGTCT	TTATTTCTTG	120
TGCTGTCTTA	CCCATCTCAA	AAGAGTGCCA	AAATCCACCA	AGTTGCTGAA	ACAGAAATCT	180

AAGAAATATC CTTGATTCTT CTTTTTCCCA TCTACTTCAC TTCTAATTCA TTAGTAAATA ATCTGTTTCA GAAAACCAAA CACCTCATGT TCTCACTCAT AAGGGGGAGT TGAACAATGA GAACACACAG ACACAGGGAG GGGAACATCA CACACCACGG CCCGTCAGGG AGTANGGGAC ATGAGTCAGT CTA	240 300 360 373
(2) INFORMATION FOR SEQ ID NO:238:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 492 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:(A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	
TAGACTGACT CATGTCCCCT ATAATGCTCC CAGGCATCAG AAAGCATCTC AAACTGGAGC TGACACCATG GCAGAGGTTT CAGGTAAGTC ACAAAAGGGG TCCTAAAGAA TTTGCCCTCA ATATCAGAGT GATTAGAAGA AGTGGACAGA GCTACCCAAG TTAAACATAT GCGAGATAAA AAAAATATGG CACTTGTGAA CACACACTAC AGGAGGAAAA TAAGGAACAT AATAGCATAT TGTGCTATTA TGATGATGAA GAACCTCTCT ANAAGAAAC ATAACCAAAG AAACAAAGAA AATTCCTGCN AATGTTTAAT GCTATAGAAG AAATTAACAA AAACATATAT TCAATGAATT CAGAAAAGTT AGCAGGTCAN AAGAAAACAA ATCAAAGACC AGAATAATCC CATTTTAGAT TGTCGAGTAA ACTANAACAG AAAGAATACC ACTGGAAATT GAATTCCTAC GTANGGGACA TGANTCANTC TA (2) INFORMATION FOR SEQ ID NO:239:	60 120 180 240 300 360 420 480 492
(A) LENGTH: 482 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(7i) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	
TGGAAAGTAT TTAATGATGG GCAACTTGCT GTTTACTTCC TACATATCCC ATCATCTTC GTATTTTTT AAATAACTTT TTTTTGGATT TTTAAAGTAA CCTTATTCTG AGAGGTAACA TGGATTACAT ACTTCTAAGC CATTAGGAGA CTCTATGTTA AACCAAAAGG AAATGTTACT AGATCTTCAT TTGATCAATA GGATGTGATA ATCATCATCT TTCTGCTCTA ATGGAAAAGT ACTANAACA TGGAACCATA ATCTTAGATG AACAACGTTA GAATTTGCAC TAATTCTACG GAATTTCAGT AATTCGGCAA ATGTCGGCA GTGACACAAC ATTTCATGAC GGGGACGCAT CTACCAACTT CTGGCGATAA GGGCCACCT TCCCTCTGTA CTTACAGTCC CATTTCATAC ACAGTCTTTG ATTAAATATT CACATTTTT CTCTACCTAA AGACCTTCAA GACCAGTACG	60 120 180 240 300 360 420 480
TA	482

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGTATCGACG TAGTGGTC	TC CCCATGTGAT	AGTCTGAAAT	ATAGCCTCAT	GGGATGAGAG	60
GCTGTGCCCC AGCCCGAC	AC CCGTAAAGGG	TCTGTGCTGA	GGTGGATTAG	TAAAAGAGGA	120
AAGCCTTGCA GTTGAGAT					180
GTCTCGGTAT AAAACCCG	AT TGTACATTTG	TTCAATTCTG	AGATAGGAGA	AAAACCACCC	240
TATGGCGGGA GGCGAGAC	AT GTTGGCAGCA	ATGCTGCCTT	GTTATGCTTT	ACTCCACAGA	300
TGTTTGGGCG GAGGGAAA	CA TAAATCTGCC	CTACGTGCAC	ATCCAGGCAT	AGTACCTCCC	360
TTTGAACTTA ATTATGAC	AC AGATTCCTTT	GCTCACATGT	ITTTTTGCTG	ACCTTCTCCT	420
TATTATCACC CTGCTCTC	CT ACCGCATTCC	TTGTGCTGAG	ATAATGAAAA	TAATATCAAT	480
AAAAACTTGA NGGAACTC	GG AGACCACTAC	GTCGATACA			519

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TGTATCGACG	TAGTGGTCTC	CACTCCCGCC	TTGACGGGGC	TGCTATCTGC	CTTCCAGGCC	60
ACTGTCACGG	CTCCCGGGTA	GAAGTCACTT	ATGAGACACA	CCAGTGTGGC	CTTGTTGGCT	120
	CAGAGGAGGG					180
AGGACGGTCA	GCTTGGTCCC	TCCGCCAAAC	ACGAGAGTGC	TGCTGCTTGT	ATATGAGCTG	240
CAGTAATAAT	CAGCCTCGTC	CTCAGCCTGG	AGCCCAGAGA	TGGTCAGGGA	GGCCGTGTTG	300
CCANACTTGG	AGCCAGAGAA	GCGATTAGAA	ACCCCTGAGG	GCCGATTACC	GACCTCATAA	360
ATCATGAATT	TGGGGGCTTT	GCCTGGGTGC	TGTTGGTACC	ANGAGACATT	ATTATAACCA	420
	TGCTGGTTCC					480
ACTACGTCCA	TACCAATCCA	CTAATTGCCN	GCCGCCTGCA	GGTTCAACCA	TATTGGGGAA	540
NAACTCCCCN	CCGCCGTTTG	GGATTGNCAT	NAACCTTTGA	AATTTTTTCC	TATTANTTGT	600
	TAAACCNTTG					660
						720
	TNAAACCCTG					771

(2) INFORMATION FOR SEQ ID NO:242:

(1) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 167 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(vi) ORIGINAL SOURCE:		
(A) ORGANISM: Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24	2:	
TGGGCACCTT CAATATCGGG CTCATCGATA ACATCACGCT		60
TCCTCTCTAG GAACCTCTGG ATTTTCAAAT TCTTTGAGGA	ATTCATCCAA ATTATCTGCC	120
TCTCCTCCTT TCCTCCTTTT TCTAAGGTCT TCTGGTACAA	GCGGTCA	167
(2) INFORMATION FOR SEQ ID NO:243:		
(2) INFORMATION FOR SEQ ID NO:243:		
(i) SEQUENCE CHARACTERISTICS:		
	*	
(A) LENGTH: 338 Base pairs (B) TYPE:/nucleicTacid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA	•	
	· + + + + + + + + + + + + + + + + + + +	
(vi) ORIGINAL SOURCE:	Control of the contro	
(A) ORGANISM: Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24	3:	
TTGGGCACCT TCAATATCTA CTGATCTAAA TAGTGTGGTT	TCACCCCTCT TCTTCCTCCC	60
TAAAAATCCT TGGCAAGAGT CAATCTCCAC TTTACAATAG		120
ATATTCTTGA CAAAGCTAGC ATAGAGACAG CAATTTTACA		180
TAATAACAGT GGTTTTCCTA CACCCATAGG GTGCCACCAA		240
GAAACAAATT AAGATACTGA AGACAACACT ACTTACCATT		300
GTTCAACTGT ACATGTATGT TCTTATGGGC AATCAAGA	• • •	338
(2) INFORMATION FOR SEQ ID NO:244:		
(i) SEQUENCE CHARACTERISTICS:	*** * _	
(A) LENGTH: 346 base pairs		
(B) TYPE: nucleic acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE - PNA		
(ii) MOLECULE TYPE: CDNA		
(vi) ORIGINAL SOURCE:		
(A) ORGANISM: Homo sapiens		
· · · · · · · · · · · · · · · · · · ·		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244	4:	

TTTTTGGCTC	CCATACAGCA	CACTCTCATG	GGAAATGTCT	GTTCTAAGGT	CAACCCATAA	60	
TGCAAAAATC	ATCAATATAC	TTGAAGATCC	CCGTGTAAGG	TACAATGTAT	TATTATATT	120	
		TACCAGTTTT				180	
					GAAAAAAGAT	240	
		ATCATGATCT			TTACTGTAAA	300	
AGGGAAGAAG	GAATGAAGAC	GAGCTAAGGA	TATTGAAGGT	GCCCAA		346	
(2) INFORMATION FOR SEQ ID NO:245:							

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

ACCAATCCCA	CACGGATACT	GAGGGACAAG	TATATCATCC	CATTTCATCC	CTACAGCAGC	60
					AGACTTAGGG	120
		GTCGCACAAT				180
		CTGCAGATTA				240
		GTCCACAAGG				300
		CAGGGTCTGC				360
		ATATGTTACA				420
		ATGCTTGTTC			TATTGAANGT	480
GCCCAAATCA	CTANTTGCGG	GCGCCTGCAN	GTCCANCATA	T		521

- (2) INFORMATION FOR SEQ ID NO:246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

TGGAACCAAT	CCAAATACCC	ATCAATGATA	GACTGGATAA	AGAAAATTTG	GCACATGTTC	60
ACCATGAAAT	ACTATGCAGC	CATAAAAAAG	GATGAGTTCA	TATCCTTTGC	AGGGACATGG	120
ATGAAGCTGG	AGACCATCAT	TCTCAGCAAA	CTAACAAGGG	AACAGAAAAC	CAAACACTGC	180
					GGAGGGGAAC	240
ATCACACAGT	GGGGCCTGCT	GGTGGGTAGG	GGTCTAGGGG	AGGGATAGCA	TTACGAGAAA	300
TACCTAATGT	AGATGACGGG	TTGATGGGTG	CAGCAAACCA	CCATGACACG	TGTATACCTA	360
TGTAACAAAC	CTGCATGTTC	TGCACATGTA	CCCCAGAACT	TAAAGTGTTA	TAAAAAAAT	420
TAAGAAAAA	GTTAAGTATG	TCATAGATAC	TTATAAATATT	GTANATATTG	AAGGTGCCCA	480

AA	482
(2) INFORMATION FOR SEQ ID NO:247:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:	
TTCGATACAG GCACAGAGTA AGCAGAAAAA TGGCTGTGGT TTAACCAAGT GAGTACAGTT AAGTGAGAGA GGGGCAGAGA AGACAAGGGC ATATGCAGGG GGTGATTATA ACAGGTGGTT GTGCTGGGAA GTGAGGGTAC TCGGGGATGA GGAACAGTGA AAAAGTGGCA AAAAGTGGTA AGATCAGTGA ATTGTACTTC TCCAGAATTT GATTTCTGGN GGAGTCAAAT AACTATCCAG TTTGGGGTAT CATANGGCAA CAGTTGAGGT ATAGGAGGTA GAAGTCNCAG TGGGATAATT GAGGTTATGA ANGGTTTGGT ACTGACTAGT ACTGACAANG TCTGGGTTAT GACCATGGGA ATGAATGACT GTANAAGCGT ANAGGATGAA ACTATTCCAC GANAAAGGGG TCCNAAAACT AAAAANNNAA GNNNNNGGGG AATATTATTT ATGTGGATAT TGAANGTGCC CAAA (2) INFORMATION FOR SEQ ID NO:248: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	60 120 180 240 300 360 420 474
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:	
TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT CCGGATGGC ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTTGCTC TGTTGATGGC CCTGAGGGGA CGCAGGACCC TTATGACCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG ATTGANTCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG TTCCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT CTCAACAGGTT TCCGATGGCT GTGATGGCA TAGTCATANT TAACCNTGTN TCGAA	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:249:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 434 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:	
TTGGATTGGT CCTCCAGGAG AACAAGGGGA AAAAGGTGAC CGAGGGCTCC CTGGAACTCA AGGATCTCCA GGAGCAAAAG GGGATGGGGG AATTCCTGGT CCTGCTGGTC CCTTAGGTCC	60 120

120

ACCCGCTGGC CAGAAAGGTG ACAGTGGTCT TCCAGGGCCT CCTGGGCCTC CAGGTCCACC TGGTGAAGTC ATTCAGCCTT TACCAATCTT GTCCTCCAAA AAAACGAGAA GACATACTGA AGGCATGCAA GCACATGCAG ATGATAATAT TCTTGATTAC TCGGATGGAA TGGAAGAAAT ATTTGGTTCC CTCAAATCCC TGAAACAAGA CATCGAGCAT ATGAAATTTC CAATGGGTAC	180 240 300 360 420 434
(2) INFORMATION FOR SEQ ID NO:250:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NC:250:	
GGAGAGGGGT GGTGCGATCT TGGCTCTCTG CAACCCCCGC CTCAAGCAAT TCTCCTGTCT TAGCCTCGCG GGTAGATGGA ATTACAGGCG CCCACCGCCA TGCCCAACTA ATTTTTTTGT GTCTTCAGTA GAGACAGGGT TTCGCCATGT TGGGCAGGCT GGTCTTGAAC TCCTGACCTC NAGTGATCTG CCCTCCTCGG CCTCACAAAG TGCTGCAATT ACAGGCATGG GCTGCTCCAC CCAGTCAACT TCTCACTAGT TATGGCCTTA TCATTTTCAC CACATTCTAT TGGCCCAAAA 4	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:251:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251: 	
GGAGTCTGTG CCGAGGTGCA GCTGRTGCAG TCTGGAGCAG AGGTGAAAAA GTCCGGGGAG 1 TCTCTGAAGA TCTCCTGTAA GGGTTCTGGA TACACCTTTA AGATCTACTG GATCGCCTGG 1 GTGCGCCAGT TGCCCGGGAA AGGCCTGGAG TGGATGGGGC TCATCTTTCC TGATGACTCT 2 GATACCAGAT ACAGCCCGTC CTTCCAAGGC CAGGTCACCA TCTCAGTCGA TAAGTCCATC 3	60 20 80 40 00 29
(2) INFORMATION FOR SEQ ID NO:252:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 536 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:	
TGGTACTCCA CTCAGCCCAA CCTTAATTAA GAATTAAGAG GGAACCTATT ACTATTCTCC	60

CAGGCTCCTC TGCTCTAACC AGGCTTCTGG GACAGTATTA GAAAAGGATG TCTCAACAAG

TATGTAGATC CTGTACTGGC CTAAGAAGTT AAACTGAGAA TTAATGGTCG TTGAGACTTG TGTCCTGGAG CAGCTGGGAT AGAGGAAGAA CTGCCTGGAA GGGGGCATCA TGTTAAAAAA GGCCCCCTTC CCAGCTCTCA GCCTAGAGTA TTAGCATTTC TCCTTGCTTA GAATGTGCCA CCGGGGGGAG TCCCTGTGGC AGAGTGGCAT CCTATCTTCT GTGTGCCCAC AGGAGCCTGC GTTTCTGGTC CAGGCTTTGC CCTTGACTCA CTATGTGACC	AGGAAAACTT TACAAGGGA TCAGCTAGAG TGATGAGGCT CCCGAGACTT	TTGGGCAGCA ACCCACACCA ACTCACAACT CTCAAGAGTG AGCAGGTGAA	180 240 300 360 420 480 536
(2) INFORMATION FOR SECTION NO: 253:	; ·		
, , , , , , , , , , , , , , , , , , ,			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 507 base pairs			
(B) TYPE: nucleic acid	***		
(C) STRANDEDNESS: single -			
(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25			
NTGTTGCGAT CCCAGTAACT CGGGAAGCTG AGGCGGGAGC			60
TGAGGCCGCA GTGAGCCGGG ACCACGCCAC TACACTCCAG			120
CCTCCAAGAC AGAAAAGAAA AGAAAGGAAG GGAAAGGGAA GGAAAAGGAA AAGGAAAAGA CAAGACTTGA			180
ATTITATOTT CTTTCTACAC CACAATTCCT CTGCTTACTA			240
CTCGTTCCAT TCTTTACAGC AAGCTGGAAG TTTGGTCAAG			300 360
AATTTGAATA TTATATGCCA GGTGTTTTTC ATTCCTGCTC	TCACTTAATT	CTCACCACTC	420
TGATATAAAT ACAATTGCTG CCGGGTGTGG TGGCTCATGC			480
			507
(2) INFORMATION FOR SEQ ID NO:254:			
(i) SEQUENCE CHARACTERISTICS:			
(A) LENGTH: 222 base pairs (B) TYPE: nucleic acid			
(C) STRANDEDNESS: single			
(D) TOPOLOGY: linear			
(=) ISTODOGIC PINCUI	•		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25	4:		
	4	1.4	
TTGGATTGGT CACTGTGAGG AAGCCAAATC GGATCCGAGA	GTCTTTTTCT	ÄAAGGCCAGT	60
ACTGGCCACA CTTTCTCCTG CCGCCTTCCT CAAAGCTGAA	GACACACAGA	GCAAGGCGCT	120
TCTGTTTTAC TCCCCAATGG TAACTCCAAA CCATAGATGG		TGCTCATCTT	180
TCCACATCCC TGCTATTCAG TATAGTCCGT GGACCAATCC	AA		222
(2) INFORMATION FOR SEQ ID NO:255:			
(i) SEQUENCE CHARACTERISTICS:			
(A) LENGTH: 463 base pairs			
(B) TYPE: nucleic acid			
(C) STRANDEDNESS: single			
(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25	ō:		
TCTTCOOLEG CAMANAGOR CANASAGOR			
TGTTGCGATC CATAAATGCT GAAATGGAAA TAAACAACAT GGGAGGGAGC ACATTAAGGT GGCCATGAAG TTTGTTGGAA			60
TOTAL DEPOSIT OF THE PROPERTY	GAAG I GACTIT	LIGAACAAGG	120

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CCTTGGTGTT AAGAGCTGAT GAGAGTGTCC CAGACAGAGG GGCCACTGGT ACAATAGACG	180
AGATGGGAGA GGGCTTGGAA GGTGTGCGAA ATAGGAAGGA GTTTGTTCTG GTATGAGTCT	240
AGTGAACACA GAGGCGAGAG GCCCTGGTGG GTGCAGCTGG AGAGTTATGC AGAATAACAT	300
TAGGCCCTGT GGGGGACTGT AGACTGTCAG CAATAATCCA CAGTTTGGAT TTTATTCTAA	360
GAGTGATGGG AAGCCGTGGA AAGGGGGTTA AGCAAGGAGT GAAATTATCA GATTTACAGT	
GATAAAAATA AATTGGTCTG GCTACTGGGG AAAAAAAAAA	420
The second of th	463
(2) INFORMATION FOR SEQ ID NO:256:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 262 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:	
TTGGATTGGT CAACCTGCTC AACTCTACYT TTCCTCCTTC TTCCTAAAAA ATTAATGAAT	60
CCAATACATT AATGCCAAAA CCCTTGGGTT TTATCAATAT TTCTGTTAAA AAGTATTATC	120
CAGAACTGGA CATAATACTA CATAATAATA CATAACAACC CCTTCATCTG GATGCAAACA	180
TCTATTAATA TAGCTTAAGA TCACTTTCAC TTTACAGAAG CAACATCCTG TTGATGTTAT	240
TTTGATGTTT GGACCAATCC AA	262
	202
(2) INFORMATION FOR SEQ ID NO:257:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 461 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:	
(MI) OLGOBREL DESCRIPTION: SEQ ID NO:257:	
GNGGNNNNNN NNNCAATTCG ACTCNGTTCC CNTGGTANCC GGTCGACATG GCCGCGGGAT	60
TACCGCTTGT NNCTGGGGGT GTATGGGGGA CTATGACCGC TTGTAGCTGG GGGTGTATGG	120
GGGACTATGA CCGCTTGTAG MTGGKGGTGT ATGGGGGGACT ATGACCGCTT GTCGGGTGGT	180
CGGATAAACC GACGCAAGGG ACGTGATCGA AGCTGCGTTC CCGCTCTTTC GCATCGGTAG	240
GGATCATGGA CAGCAATATC CGCATTCGYC TGAAGGCGTT CGACCATCGC GTGCTCGATC	300
AGGCGACCGG CGACATCGCC GACACCGCAC GCCGTACCGG CGCGCTCATC CGCGGTCCGA	360
TCCCGCTTCC CACGCGCATC GAGAAGTTCA CGGTCAACCG TGGCCCGCAC GTCGACAAGA	420
AGTCGCGCGA GCAGTTCGAG GTGCGTACCT ACAAGCGGTC A	461
(2) INFORMATION FOR SEQ ID NO:258:	
Tok one in No.238.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 332 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:	
TGACCGCTTG TAGCTGGGGG TGTATGGGGG ACTACGACCG CTTGTAGCTG GGGGTGTATG	60
GGGGACTATG ACCGCTTGTA GCTGGGGGTG TATGGGGGGAC TATGACCGCT TGTAGCTGGG	120
GGTGTATGGG GGACTAGGAC CGCTTGTAGC TGGGGGTGTA TGGGGGACTA TGACCGCTTG	180
IOOOOOACIA IOACCGCIIG	TOO

TAGCTGGGGG TGTATGGGGG ACTACGACCG CTTGTAGCTG GGGGTGTATG GGGGACTATG ACCGCTTGTA NCTGGGGGTG TATGGGGGAC TATGACCGCT TGTGCTGCCT GGGGGATGGG AGGAGAGTTG TGGTTGGGGA AAAAAAAA	240 300 332
(2) INFORMATION FOR SEQ ID NO:259:	2.72
(i) CEOUDING CANDAGED CONTRACTOR	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:	
(XI) SECOUNCE DESCRIPTION: SEQ ID NO: 259:	
TACCGCTTGT GACCGCTTGT GACCGCGTGT GACCGCTTGT GACCGCGTGT GACCGCTTGT GACCACTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCACTTGT GACCACTTGT GACCACTTGT	60 120 180 240
GTGCNNCCTG GGGGATCNGA GGAGANTNGN GGNTAGNGAT GGTTNGGGAN A	240
(2) INFORMATION FOR SEQ ID NO: 260:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 238 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(with GEOURNOE DEGOETER-Town and a	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:	
TAAGAGGGTA CTGGTTAAAA TACAGGAAAT CTGGGGTAAT GAGGCAGAGA ACCAGGATAC	60
TTTGAGGTCA GGGATGAAAA CTAGAATTTT TTTCTTTTTT TTTGCCTGAG AAACTTGCTG	120
CTCTGAAGAG GCCCATGTAT TAATTGCTTT GATCTTCCTT TTCTTACAGC CCTTTCAAGG	180
GCAGAGCCCT CCTTATCCTG AAGGAATCTT ATCCTTAGCT ATAGTATGTA CCCTCTTA	238
(2) INFORMATION FOR SEQ ID NO:261:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 746 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(b) Torobodi. Timear	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:261:	
TTGGGCACCT TCAATATCAA TAGCTAACAT TTATTGAGTG TTTATCGTAT CATAAAACAC	60
GTTCTAAGC CTTTAAACGT ACTAATTCAT TTAATGCTCA TAATCACTTT AGAAGGTGGG	120
PACTAGTATT AGTCTCATTT ACAGATGCAA CATGCAGGCA CAGAGAGGTT AATTAACTTG	180
CCAAGSTAA CACAGCTAAG AAATAGAAAA AATATTGAAT CTGGAAAGTT GGGCTTCTGG	240
STAACCCACA GAGTCTTCAA TGAGCCTGGG GCCTCACTCA GTTTGCTTTT ACAAAGCGAA	300
GAGTAACAT CACTTAATTC AGTGAGTAGG CCAAATGGAG GTCAGCTACG AGTTTCTGCT	360
TTCTTGCAG TGGACTGACA GATGTTTACA ACGTCTGGCC ATCAGTWAAT GGACTGATTA	420
CATTGGGAW GTGGGTGGGC TGAATGTTGG CCAGTGAAGT TTATTCAWGC CATATTTTTA	480
GTTTAGGAT GACTTTTGGC TGGTCCTAGG GCAAGCTCTG TCTGSCACGG AACACAGAAT	540
IACACAGGGA CCCCCTCAAT TTCTGGTGTC GCTAAAAGGA TGAAGGA GTG GTTGGGGGGA	

CAAGCGGTCA	AAACCTAAGT	GCGGCCGGCT	GGCAGGGTCC	ACCCATATGG	GGAAAACTCC	660
CNACGCGTTT	GGAATGCCTN	AGCTNGAATT	ATTCTAANAG	TTGTCCNCNT	AAAATTAGCC	720
TGGGCGTTAA	TCANGGGTCN	NAAGCC				746

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

				CCTTTGTAGG		60
TTTGTCTGTT	TCTTCTTTCT	CTTTTCCTTC	CCATATCCTC	CTAATTTACG	TTTGACTTGT	120
TTGCTGAGGA	GGCAGGAGCT	AGAGACTGCT	GTGAGCTCAT	AGGGGTGGGA	AGTTTATCCT	180
TCAAGTCCCG	CCCACTCATC	ACTGCTTCTC	ACCTTCCCCT	GACCAGGCTT	ACAAGTGGGT	240
TCTTGCCTGC	TTTCCCTTTG	GACCCAACAA	CCCCTGTAA	TGAGTGTGCA	TGACTCTGAC	300
AGCTGTGGAC	TCAGGGTCCT	TGGCTACAGC	TGCCATGTAA	AATATCTCAT	CCAGTTCTCG	360
CAAATTGTTA	AAATAACCAC	ATTTCTTAGA	TTCCAGTACC	CAAATCATGT	CTTTACGAAC	420
TGCTCCTCAC	ACCCAGAAGT	GGCACAATAA	TTCTTGGGGA	ATTATTACTT	TTTTTTTCT	480
CTCTNTTNNC	GNNNCNNNNG	GNNNGNCCAG	GAATTACCAC	NTTGGAAGAC	CTGGCCNGAA	540
TTTATTATAN	AGGGGAGCCG	ATTNTTTTTC	CTAACACAAA	GCGGGTCA		588

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 730 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTTTTTTTT TTTGGCCTGA GCAACTGAAA TTATGAAATT TCCATATACT CAAAAGAGTA	60
AGACTGCAAA AAGATTAAAT GTAAAAGTTG TCTTGTATAC AGTAATGTTT AAGATACCTA 1	20
TTANATTTAT AAATGGAAAA TTAGGGCATT TGGATATACA AGTTGAAAAT TCAGGAGTGA 1	80
GGTTGGGCTG GCTGGGTATA TACTGAAAAC TGTCAGTACA CAGATGACAT CTAAAACCAC 2	40
AAATCTGGTT TTATTTTAGC AGTGATATGT GTCACTCCCA CAAAAGCCTT CCCAATTGGC 3	00
CTCAGCATAC ACAACAAGTC ACCTCCCCAC AGCCCTCTAC ACATAAACAA ATTCCTTAGT 3	60
TTAGTTCAGG AGGAAATGCG CCCTTTTCCT TCCGCTCTAG GTGACCGCAA GGCCCAGTTC 4	20
TCGTCACCAA GATGTTAAGG GAAGTCTGCC AAAGAGGCAT CTGAAAGGAA ATAAGGGGAA 4	80
	40
CATTTCACAA CAAAACTCNG GAACAAACCT TGTCTCATCA ATCATTTAAG CCCTTCGTTT 6	00
GGANNAGACT TTCTGAACTG GGCGCTGAAC ATAANCCTCA TTGAATGTCT TCACAGTCTC 6	60
CCAGCTGAAG GCACACCTTG GGCCAGAAGG GGAATCTTCC AGGTCCTCAA NACAGGGCTC 7	20
GCCCTTTGNC 7	30

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 715 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TTTTTTTTT	TTTGGCCAGT	ATGATAGTCT	CTACCACTAT	ATTGAAGCTC	TTAGGTCATT	60
		ATGCTGTTGA				120
GTCTCTTTTT	TGTTCCTTTT	CTCTTCTTTT	CCTCCCTTAT	TTTATAATTG	AATTTTTTAG	180
GATTCTATTT	TATATAGATT	TATCAGCTAT	AACACTTTGT	ATTCTTTTGT	TTTGTGGTTC	240
TTCTGTCATT	TCAATGTGCA	TCTTAAACTC	ATCACAATCT	ATTTTCAAAT	AATATCATAT	300
AACCTTACAT	ATAATGTAAG	AATCTACCAC	CATATATTTC	CATTTCTCCC	TTCCATCCTA	360
TGTNTGTCAT	ATTTTTTCCT	TTATATATGT	TTTAAAGACA	TAATAGTATA	TGGGAGGTTT	420
TTGCTTAAAA	TGTGATCAAT	ATTCCTTCAA	NGAAACGTAA	AAATTCAAAA	TAAATNTCTG	480
TTTATTCTCA	AATNNACCTA	ATATTTCCTA	CCATNTCTNA	TACNTTTCAA	GAATCTGAAG	540
GCATTGGTTT	TTTCCGGCTT	AAGAACCTCC	TCTAAAGCAC	TCTAAGCAGA	ATTAAGTCTT	600
CTGGGAGAGG	AÄŤTCTCCCA	AGCTTGGGCC	TTNANNTGTA	CTCCNTNANG	GTTAAANTTT	660
GGCCGGGAAA	TAGAAATTCC	AAGTTAACAG	GNTANTTTTT	NTTTTTTTNTTN	TCNCC	715

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid'
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TTTTTTTTT	TTTCCCAACA	CAAAGCACCA	TTATCTTTCC	TCACAATTTT	CAACATAGTT	60
TGATTCCCAT	GAAGAGGTTA	TGATTTCTAA	AGAAAACATG	GCTACTATAC	TATCAATCAG	120
GGTTAAATCT	TTTTTTTTTG	AGACGGAGTT	TA			152

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TAAACTCCGT	CCCCTTCTTA	ATCAATATGG	AGGCTACCCA	CTCCACATTA	CCTTCTTTTC	60
AAGGGACTGT	TTCCGTAACT	GTTGTGGGTA	TTCACGACCA	GGCTTCTAAA	CCTCTTAAAA	120
CTCCCCAATT	CTGGTGCCAA	CTTGGACAAC	ATGCTTTTTT	TTTTTTTTT	TTTTTTTTN	180
GAGACGGAGT	TTA					193

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TGTTGCGATC CCTTAAGCAT GGGTGCTATT AAAAAAATGG TGGAGAAGAA AATACCTGGA	6
ATTTACGTCT TATCTTTAGA GATTGGGAAG ACCCTGATGG AGGACGTGGA GAACAGCTTC	120
TTCTTGAATG TCAATTCCCA AGTAACAACA GTGTGTCAGG CACTTGCTAA GGATCCTAAA	180
TTGCAGCAAG GCTACAATGC TATGGGATTC TCCCAGGGAG GCCAATTTCT GAGGGCAGTG	240
GCTCAGAGAT GCCCTTCACC TCCCATGATC AATCTGATCT CGGTTGGGGG ACAACATCAA	300
GGTGTTTTTG GACTCCCTCG ATGCCCAGGA GAGAGCTCTC ACATCTGTGA CTTCATCCGA	360
AAAACACTGA ATGCTGGGGC GTACTCCAAA GTTGTTCAGG AACGCCTCGT GCAAGCCGAA	420
TACTGGCATG ACCCATAAAA GGAGGATGTG GATCGCAACA	460
(2) INFORMATION FOR SEQ ID NO:268:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 533 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:	
TGTTGCGATC CGTTGATAGA ATAGCGACGT GGTAATGAGT GCATGGCACG CCTCCGACTT	60
ACCTTCGCCC GTGGGGACCC CGAGTACGTC TACGGCGTCG TCACTTAGAG TACCCTCTGG	120
ACGCCCGGGC GCGTTCGATT TACCGGAAGC GCGAGCTGCA GTGGGCTTGC GCCCCCGGCC	180
AAATTCTTTG GGGGGTTTAA GGCCGCGGGG AATTTGAGGT ATCTCTATCA GTATGTAGCC	240
AAGTTGGAAC AGTCGCCATT CCCGAAAICG CTTTCTTTGA ATCCGCACCG CCTCCAGCAT	300
TGCCTCATTC ATCAACCTGA AGGCACGCAT AAGTGACGGT TGTGTCTTCA GCAGCTCCAC	360
TCCATAACTA GCGCGCTCGA CCTCGTCTTC GTACGCGCCA GGTCCGTGCG TGCGAATTCC	420
CAACTCCGGT GAGTTGCGCA TTTCAAGTTN CGAAACTGTT CGCCTCCACN ATTTGGCATG	480
TTCACGCATG ACACGGAATA AACTCGTCCA GTACCGGGAA TGGGATCGCA ACA	533
(2) INFORMATION FOR SEQ ID NO:269:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 50 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:	
TTTTTTTTT TTCGCCTGAA TTAGCTACAG ATCCTCCTCA CAAGCGGTCA	50
(2) INFORMATION FOR SEQ ID NO:270:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 519 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS. single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:	
TGTTGCGATC CALATAACCC ACCAGCTTCT TGCACACTTC GCAGAAGCCA CCGTCCTTTG	60
GCTGAGTCAC GTGAACGGTC AGTGCAAGCA GCCGCGTGCC AGAGCAGAGG TGCAGCATGC	120
TGCACACCAG CTCAGGGCTG ACCTCCTCCA GCAGGATGGA CAGGATGGAG CTGCCGTACG	180

360

TGTCCACCAC CTCCTGGCAC TCTTCCGACA GGGACTTCGG CAGCTTCGAG CACATTTTGT	240
CAAAAGCGTC GAGTATTTCT TTCTCAGTCT TGTTGTTGTC AATCAGCTTG GTCACCTCCT	300
TCACCAGGAA TTCACACACC TCACAGTAAA CATCAGACTT TGCTGGGACC TCGTGCTTCT	360
TAATGGGCTC CACCAGTTCC AGGGCAGGGA TGACATTCTT GGAGGCCACT TTGGCGGGGA	420
CCAGAGTCTG CATGGGCATC TCTTTCACCT CATCACAGAA CCCAACCAGC GCACAGATCT	
CCTTGGGTTG CATGTGCATC ATCATCTGGG ATCGCAACA	519
(2) INFORMATION FOR SEQ ID NO:271:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 457 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(X1) SEQUENCE DESCRIPTION: SEQ ID NO:271:	
TTTTTTTTT TTCGCCCGC GACCGGACGT GCACTCCTCC AGTAGCGGCT GCACGTCGTG	60
CCAATGGCCC GCTATGAGGA GGTGAGCGTG TCCGGCTTCG AGGAGTTCGA CCGGGCCGTG	120
GAACAGCACA ATGGCAAGAC CATTTTCGCC TACTTTACGG GTTCTAAGGA CGCCGGGGGG	180
AAAAGCTGGT GCCCCGACTG CGTGCAGGCT GAACCAGTCG TACGAGAGGG GCTGAAGCAC	240
ATTAGTGAAG GATGTGTTT CATCTACTGC CAAGTAGGAG AAGAGCCTTA TTGGAAAGAT	
CCAAATAATG ACTTCAGAAA AAACTTGAAA GTAACAGCAG TGCCTACACT ACTTAAGTAT	
GGAACACCTC AAAAACTGGT AGAATCTGAG TGTCTTCAGG CCAACCTGGT GGAAATGTTG	
TTCTCTGAAG ATTAAGATTT TAGGATGGCA ATCAAGA	457
(2) INFORMATION FOR SEQ ID NO:272:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 102 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:	
TTTTTTTTT TTGGGCAACA ACCTGAATAC CTTTTCAAGG CTCTGGCTTG GGCTCAAGCC	60
CGCAGGGGAA ATGCAACTGG CCAGGTCACA GGGCAATCAA GA	102
(2) INFORMATION FOR SEQ ID NO:273:	
, , , , , , , , , , , , , , , , , , ,	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 455 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:	
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	60
TTTTTTTTT TTGGCAATCA ACAGGTTTAA GTCTTCGGCC GAAGTTAATC TCGTGTTTTT	
GGCAATCAAC AGGTTTAAGT CTTCGGCCGA AGTTAATCTC GTGTTTTTGG CAATCAACAG	
GTTTAAGTCT TCGGCCGAAG TTAATCTCGT GTTTTTGGCA ATCAACAGGT TTAAGTCTTC	180
GGCCGAAGTT AATCTCGTGT TTTTGGCAAT CAACAGGTTT AAGTCTTCGG CCGAAGTTAA	240

TCTCGTGTTT TTGGCAATCA ACAGGTTTAA GTCTTCGGCC GAAGTTAATC TCGTGTTTTT

GGCAATCAAG AGGTTTAAGT CTTCGGCCGA AGTTAATCTC GTGTTTTTGG CAATCAACAG

GTTTAAGTCT TCGGCCGAAN TTAATCTCGT GTTTTTGGCA ATCAACAGGT TTAANTCTTC	420
GGCCGAAGTT AATCTCGTGT TTTTGGCAAT CAANA	455
(2) INFORMATION FOR SEQ ID NO:274:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 461 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:	
TTTTTTTTT TTGGCCAATA CCCTTGATGA ACATCAATGT GAAAATCCTC GGTAAAATAC	60
TGGCAAACCA AATCCAGCAG CACATCAAAA AGCTTATCCA CCATGATCAA GTGGGCTTCA	120
TCCCTGGGAT GCAACGCTGG TTCAACATAA GAAAATCAAT AAATGTAATC CATCACATAA	180
ACAGAACCAA AGACAAAAAC CACATGATTA TCTCAATAGA TGCAGAAAAG GCCTTGGACA	240
AATTCAACAG CCCTTCATGC TAAACACTCT TAATAAACTA GATATTGATG GAATGTATCT	300
CAAAATAATA AGAGCTATTT ATGACAAACC CACAGCCAAT ATCATACTGA ATGGGCAAAG	360
ACTGGAAGCA TTCCCTTTGA AAACTGGCAC AAGACAAGGA TGCCCTCTCT CACCGCTCCT	420
ATTCAACATA GTATTGGAAG TTCTGGCCAG GGCAATCAAG A	461
(2) INFORMATION FOR SEQ ID NO.275:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 729 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:	
TTTTTTTTTT TTGGCCAACA CCAAGTCTTC CACGTGGGAG GTTTTATTAT GTTTTACAAC	60
CATGAAAACA TAGGAAGGTG GCTGTTACAG CAAACATTTC AGATAGACGA ATCGGCCAAG	120
CTCCCCAAAC CCCACCTTCA CAGCCTCTTC CACACGTCTC CCANAGATTG TTGTCCTTCA	180
CTTGCAAATT CANGGATGTT GGAAGTNGAC ATTTNNAGTN GCNGGAACCC CATCAGTGAA	240
NCANTAAGCA GAANTACGAT GACTTTGANA NACANCTGAT GAAGAACACN CTACNGANAA	300
CCCTTTCTNT CGTGTTANGA TCTCNNGTCC NTCACTAATG CGGCCCCCTG CNGGTCCACC	360
ATTTGGGAGA ACTCCCCCN CGTTGGATCC CCCCTTGAGT NTCCCATTCT NGTCCCCCAN ACCNGNCTTG NGNGNCANTN CNNCCTCNCA CCNTGTTTCC CTGNNGTNAA AATNNGTTTT	420
NCCGCCNCCC NAATTCCCAC CCNAATCACA GCGAANCCNG AAGGCCTTCN NAAGTGTTTA	480
ANGCCCNGNG GTTTCCTCNT NTANTTGCAG CCTACCCTCC CNCTTNNNNT TNCGNGTTGG	540
TCGCGCCCTG GNCNCGCCTN GTTCCTCTTT NNGGNNACAA CCTNGNTCNN NGGCNCNTCN	600
NNNCTNTTCC TNNNACTAGC TNGCCTNTCC NCNCCGNGGN NCANNGCACA TTNCNCNNAC	660
INTGTNNCC	720
	729
(2) INFORMATION FOR SEQ ID NO:276:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

300

360

420

452

TGACCTGACA TGTAGTAGAT ACTTAATAAA TATTTGTGGA ATGAATGGAT GAAGTGGAGT	60
TACAGAGAAA AATAGAAAAG TACAAATTGT TGTCAGTGTT TTGAAGGAAA ATTATGATCT	120
TTCCCAAAGT TCTGACTTCA TTCTAAGACA GGGTTAGTAT CTCCATACAT AATTTTACTT	180
GCTTTTGAAA ATCAAATGAG ATAATCTATT TAGATTGATA ATTTATTTAG ACTGGCTATA	240
AACTATTAAG TGCTAGCAAA TATACATTTT AATCTCATTT TCCACCTCTT GTGATATAGC	300
TATGTAGGTG TTGACTTTAA TGGATGTCAG GTCAATCCC	339
(2) INFORMATION FOR SEQ ID NO:277:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 664 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:	
(XI) SEQUENCE DESCRIPTION. SEQ ID NO:277:	
TGACCTGACA TCCATAACAA AATCTTTCTC CATTATATTC TTCTAGGGGA ATTTCTTGAA	60
AAGCATCCAA AGGAAACLAA TGATGGTAAG ACCGTGCCAA GTGGGGAGCA GACACCAAAG	120
TAAGACCACA GATTTTACAT TCAACAGGTA GCTCACAGTA CTTTGCCCGA CACTGTGGGC	180
AGAAATAGCC TCCTAATGTA AGCCCTGGCT CAGTATTGCC ATCCAAATGC GCCATGCTGA	240
AAGAGGGTTT TGCATCCTGG TCAGATNAAG AAGCAATGGT GTGCTGAGGA AATCCCATAC	300
GAATAAGTGA GCATTCAGAA CTTGAGCTAG CAGGAGGAGG ACTAAGATGA TGTGTGAGCA	360
ACTCTTTGTA ATGGCTTTCA TCTAAAATAA CATGGTACGT GCCACCAGTT TCACGAGCAA	420
GTACAGTGCA AACGCGAACT TCTGCAGACA ATCCAATAAC AGATACTCTA ATTTTAGCTG	480
CCTTTAGGGT CTTGATTAAA TCATAAATAT TAGATGGATC GCAAGTTGTA AGGNTGCTAA	540
AAGATGATTA GTACTTCTCG ACTTGTATGT CCAGGCATGT TGTTTTAAAN TCTGCCTTAG	600
NCCCTGCTTA GGGGAATTTT TAAAGAAGAT GGCTCTCCAT GTTCANGGTC AATCACNAAT	660
TGCC	664
(2) INFORMATION FOR SEQ ID NO:278:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 452 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:	
TCACCTCACA TTCACCAACA COACA COACACATT COACACAT	
TGACCTGACA TTGAGGAAGA GCACACCCT CTGAAATTCC TTAGGTTCAG AAGGGCATTT	60
GACACAGAGT GGGCCTCTGA TAATTCATGA AATGCATTCT GAAGTCATCC AGAATGGAGG	120
CTGCAATCTG CTGTGCTTTG GGGGTTGCCT CACTGTGCTC CTGGATATCA CACAAAAGCT	180
GCAATCCTTC TTCTTCAACT AACATTTTGC AGTATTTGCT GGGATTTTTA CTGCAGACAT	240

GATACATAGC CCATAGTGCC CAGAGCTGAA CCTCTGGTTG AGAGAAGTTG CCAAGGAGCG

GGAAAAATGT CTTGAAAGAT CTATAGGTCA CCAATGCTGT CATCTTACAA CTTGAACTTG

GCCAATTCTG TATGGTTGCA TGCAGATCTT GGAGAAGAGT ACGCCTCTGG AAGTCACGGG

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid

ATATCCAAAN CTGTCTGTCA GATGTCAGGT CA

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:	
TTTTTTTTT TTCGGCAAGG CAAATTTACT TCTGCAAAAG GGTGCTGCTT GCACTTTTGG CCACTGCGAG AGCACCCAA ACAAAGTAGG GAAGGGGTTT TTATCCCTAA CGCGGTTATT CCCTGGTTCT GTGTCGTGTC	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:280:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 272 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:	
TACCTGACAT GGAGAATAA CTTGTAGTAT TTTGCGTGCA ATGGAATACT ATATGAGGGT GAAAATGAAT GAACTAGCAA TGCGTGTATC AACATGAATA AATCCCCAAA ACATAATAAT GTTGAATGGA AAAGGTGAGT TTCACAACGA TATATATGCC CTCTAAATCC ATTTATGTAA ACCTTTAAAA AACTACATTA TTTATGGTCA TAAGTCCATC CAGAAAATAT TTAAAAACCT ACATGGGATT GATAACTACT GATGTCAGGT CA	60 120 180 240 272
(2) INFORMATION FOR SEQ ID NO:281:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 431 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:	
TTTTTTTTT TTGGCCAATA GCATGATTA AACATTGGAA AAAGTCAAAT GAGCAATGCG AATTTTATG TTCTCTTGAA TAATCAAAAG AGTAGGCAAC ATTGGTTCCT CATTCTTGAA TAGCATTAAT CAGAAAATAT TGCATAGCCT CTAGCCTCCT TAGAGTAGGT GTGCTCTCC AAATATATCA TAGTCCCACA GTTTATTTCA TGTATATTTT CTGCCTGAAT CACATAGACA TTTGAATTTG CAACGCCTGA TGTAAATATA TAAATTCTTA CCAATCAGAA ACATAGCAAG AAATTCAGGG ACTTGGTCAT YATCAGGGTA TGACAGCANA TCCCTGTARA AACACTGATA CACACTCACA CACGTATGCA ACGTGGAGAT GTCGCYTTWW KKKTWYWCWM RMRYCRWCGN AATCACTTAN N	60 120 180 240 300 360 420 431
(2) INFORMATION FOR SEQ ID NO:282:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATTCGATTCG ATGCTTGAGC CCAGGAGTTC AAGACTGCAG TGAGCCACTG (TGGACAACAG AGCGAGTCCC TGTGCCAAAA AAAAAAAA	CACTTCAGGC 60 98
(2) INFORMATION FOR SEQ ID NO:283:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 764 base pairs(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:	
TTTTTTTTT TTCGCAAGCA CGTGCACTTT ATTGAATGAC ACTGTAGACA	GGTGTGTGGG 60
TATAAACTGC TGTATCTAGG GGCAGGACCA AGGGGGCAGG GGCAACAGCC (CCAGCGTGCA 120
GGGCCASCAT TGCACAGTGG ASTGCAAAGG TTGCAGGCTA TGGGCGGCTA	
CGTTTTTCCT GTATTATCTG TAACATAATA TGGTAGACTG TCACAGAGCC (
HACASGATGA ATCCAAWGGT CAYGAGGATG CCCASAATCA GGGCCCASAT	
TTGGCGGTGG GGGCATASGC CTGKGCCCCG GTCACGTCSC CAACCWTCTY (
CMCTTGAWTC CNCNCCTTNN NNTNCCNTNA TNTGCCCGCC CNCCTCCTNG I	NGTCAACCNG 420 NTTATCCTTN 480
NATCTGCACT ANCTCCCTCN CCCCTTNTGGT ANTCTCNTCC TTCAANTAAN ACNCCCCCT CNCCTTTCCC CTNCCNCCCN TNATCCCNGN NCCNCTATCA	
CUCTUTUCTU CUNATCGTTC CUCCTUUTAA CTACUCTTU NACUAUNCCT	CACTNATNCC 600
NGNNANTTCT TTCCTTCCCT CCCNACGCNN TGCGTGCGCC CGTCTNGCCT	
CCCNNACTTT ATTTACCTTT NCACCCTAGC NCTCTACTTN ACCCANCCNC	
NGGNCCACCC NNCCCTNATC NCTNNCTCTN TCNNCTCNTT CCCC	764
: **	
(2) INFORMATION FOR SEQ ID NO:284:	
(i) SEQUENCE CHARACTERISTICS:	
(1) SEQUENCE CHARACTERISTICS. (A) LENGTH: 157 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:	
CAAGTGTAGG CACAGTGATG AAAGCCTGGA GCAAACACAA TCTGTGGGTA	
ATTTCTCCCC TTCCAGGAAC GTCTTGCATG GATGATCAAA GATCAGCTCC	
AAATAAGCTA GTTTAAGATA CGTTCCCCTA CACTTGA	157
(2) INFORMATION FOR SEQ ID NO:285:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 150 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:	* (
ATTCGATTGT ACTCAGACAA CAATATGCTA AGTGGAAGAA GTCAGTCACA	
TACTGTATGA CTTCATTTAC ATTAAGTGTC CAGAATAGGC AAATCCGTAG TAGATGAGCA GCTGCCTAGG TCTGAGTACA	

(2) INFORMATION FOR SEQ ID NO:286:

134

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 219 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:	
ATTCGATTT TTTTTTTTG GCCATGATGA AATTCTTACT CCCTCAGATT TTTTGTCTGG ATAAATGCAA GTCTCACCAC CAGATGTGAA ATTACAGTAA ACTTTGAAGG AATCTCCTGA GCAACCTTGG TTAGGATCAA TCCAATATTC ACCATCTGGG AAGTCAGGAT GGCTGAGTTG CAGGTCTTTA CAAGTTCGGG CTGGATTGGT CTGAGTACA	60 120 180 219
(2) INFORMATION FOR SEQ ID NO:287:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:	
ATTCGATTCT TGAGGCTACC AGGAGCTAGG AGAAGAGGCA TGGAACAAAT TITCCCTCAT ATCCATACTC AGAAGGAACC AACCCTGCTG ACACCTTAAT TTCAGCTTCT GGCCTCTAGA ACTGTGAGAG AGTACATTTC TCTTGGTTTA AGCCAAGAGA ATCTGTCTTT TGGTACTTTA TATCATAGCC TCAAGA	60 120 180 196
(2) INFORMATION FOR SEQ ID NO:288:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:	
ATTCGATTTC AGTCCAGTCC CAGAACCCAC ATTGTCAATT ACTACTCTGT ARAAGATTCA TTTGTTGAAA TTCATTGAGT AAAACATTTA TGATCCCTTA ATATATGCCA ATTACCATGC TAGGTACTGA AGATTCAAGT GACCGAGATG CTAGCCCTTG GGTTCAAGTG ATCCCTCTCC CAGAGTGCAC TGGACTGAA	60 120 180 199
(2) INFORMATION FOR SEQ ID NO:289:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:	

ATTCGATTCT	TGAGGCTACA	AACCTGTACA	GTATGTTACT	CTACTGAATA	CTGTAGGCAA	60
					TGAAACTTCA	120
					AAAAAAAAA	180
AA						182

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCACGAGGA	GAAATGTAAT	TCCATATTTT	ATTTGAAACT	TATTCCATAT	TTTAATTGGA	60
TATTGAGTGA	TTGGGTTATC	AAACACCCAC	AAACTTTAAT	TTTGTTAAAT	TTATATGGCT	120
	AGTATAAGTT		TTTGATAACA	TTGAAAGATA	GTATTTTACC	180
ATCTTTAATC	ATCTTGGAAA	ATACAAGTCC	TCTGAACAAC	CACTCTTTCA	CCTAGCAGCA	240
TGAGGCCAAA	AGTAAAGGCT	ATATTAAATT	ACATATGGGA	TTCTTAGTAG	TATGTTTTTT	300
TCTTGAAACT	CAGTGGCTCT	ATCTAACCTT	ACTATCTCCT	CACTCTTTCT	CTAAGACTAA	360
ACTCTAGGCT	CTTAAAAATC	TGCCCACACC	AATCTTAGAA	GCTCTGAAAA	GAATTTGTCT	420
TTAAATATCT	TTTAATAGTA	ACATGTATTT	TATGGACCAA	ATTGACATTT	TCGACTATTT	480
	AGTCAGGTGA	ATTTCAGCAC	. ACTGAGTTGG	GAATTTCTTA	TCCCAGAAGA	540
CCAACCAATT	TCATATTTAT	TTAAGATTGA	TTCCATACTC	CGTTTTCAAG	GAGAATCCCT	600
GCAGTCTCCT	TAAAGGTAGA	ACAAATACTT	TCTATTTTT	TTTCACCATT	GTGGĢATTGG	660
			AACAAATATG		ATTAAGCACG	720
GACCCATATT				TGCACCTTTT		780
CTTTTCAATG				ACAAAATAAA	TAAAACTTGT	840
		GGGGTGGACA	TTGTATGTGT	AAATTAAA	CCCTGTATCA	900
	GTTGTATGGG	TCAGAGAAAA	TGAATGCTTA	GAAGCTGTTC	ACATCTTCAA	960
	AAACCACATG	TCTCAGCTAT	ATTATTATTT	ATTTTTTATG	CATAAAGTGA	1020
ATCATTTCTT	CTGTATTAAT	TTCCAAAGGG	TTTTACCCTC	TATTTAAATG	CTTTGAAAAA	1080
	ACAATGGGTT	GATATTTTTC	TTTAAAAGAA	AAATATAATT	ATGAAAGCCA	1140
	AAGCCTGTTT	TATTTTAAAA	CTTTTTATGT	TCTGTGGTTG	ATGTTGTTTG	1200
TTTGTTTGTT	TCTATTTTGT	TGGTTTTTTA	CTTTGTTTTT-	TGTTTTGTTT	TGTTTTGTTT	1260
	ATGCAGTTCT	TTAACCAATG	TCTGTTTGGC	TAATGTAATT	AAAGTTGTTA	1320
	GTGCATTTCA		TGGTTTCTTA		TGTAGAAGTA	1380
CTGGTAATTT		AATATGTTTA	AAGAGATAAC	AGTTTGATAT	GTTTTCATGT	1440
GTTTATAGCA		ATTTCTATGG	CATTCCAGCG		TGTTTGCGAG	1500
				AGCAACGCCT		1560
TTGGCCTTAT			TGGGATGTAT	TTTTTATTTT '	AAAAAAAT	1620
AAAAAAAA	AAAAAAAA	AAAAA				1646

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	50
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAG I'AGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	350
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780
TTTGCTTGTC	CCTCTTGTTC	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTTCTGG	840
GGACTTTACC	CCACCAGGCA	GCTCTGTGGA	GCTTGTCCAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CA DBAAGGCG	CTGTCATCGT	AGTCTCCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCCTG	CAGCAGGGGA	AGCAGTGGCA	GCACCACTTG	CACCTCTTGC	TCCCAAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTGCCCACG	TTGCTCTTGC	CGCTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTCAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATTCACAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTACT	GAAATCATGT	CATCTGCGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAAT	1380
AATATAATTT	TCCTCTGGAG	CCATATGGAT	GAACTATGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCCTCAGCC	ATCAGCGCCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGAT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAA	1620
TCACATAAAC	AGAATTAAAA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAA	TCCAGCATCC	TTGTATTTAT	${\tt TGTTGCAGTT}$	CTCAGAGGAA	ATGCTTCTAA	1740
CTTTTCCCCA	TTTAGTATTA	TGTTGCCTGT	GGGCTTGTCA	TAGGTGGTTT	TTATTACTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTTGCT	GAGGGTTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1851 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	€0
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780

TTTGCTTGTC CCTCTTGTTC ACATCCGTGT CCCTGAGCAT GACGATGAGA TCCTTTCTGG	840
GGACTTTACC CCACCAGGCA GCTCTGTGGA GCTTGTCCAG ATCTTCTCCA TGGACGTGGT	900
ACCTGGGATC CATGAAGGCG CTGTCATCGT AGTCTCCCCA AGCGACCACG TTGCTCTTGC	960
CGCTCCCCTG CAGCAGGGGA AGCAGTGGCA GCACCACTTG CACCTCTTGC TCCCAAGCGT	1020
CTTCACAGAG GAGTCGTTGT GGTCTCCAGA AGTGCCCACG TTGCTCTTGC CGCTCCCCCT	1080
GTCCATCCAG GGAGGAAGAA ATGCAGGAAA TGAAAGATGC ATGCACGATG GTATACTCCT	1140
CAGCCATCAA ACTTCTGGAC AGCAGGTCAC TTCCAGCAAG GTGGAGAAAG CTGTCCACCC	1200
ACAGAGGATG AGATCCAGAA ACCACAATAT CCATTCACAA ACAAACACTT TTCAGCCAGA	1260
CACAGGTACT GAAATCATGT CATCTGCGGC AACATGGTGG AACCTACCCA ATCACACATC	1320
AAGAGATGAA GACACTGCAG TATATCTGCA CAACGTAATA CTCTTCATCC ATAACAAAAT	1380
AATATAATTT TCCTCTGGAG CCATATGGAT GAACTATGAA GGAAGAACTC CCCGAAGAAG	1440
CCAGTCGCAG AGAAGCCACA CTGAAGCTCT GTCCTCAGCC ATCAGCGCCA CGGACAGGAR	1500
TGTGTTTCTT CCCCAGTGAT GCAGCCTCAA GTTATCCCGA AGCTGCCGCA GCACACGGTG	1560
GCTCCTGAGA AACACCCCAG CTCTTCCGGT CTAACACAGG CAAGTCAATA AATGTGATAA	1620
TCACATAAAC AGAATTAAAA GCAAAGTCAC ATAAGCATCT CAACAGACAC AGAAAAGGCA	1680
TTTGACAAAA TCCAGCATCC TTGTATTTAT TGTTGCAGTT CTCAGAGGAA ATGCTTCTAA	1740
CTTTTCCCCA TTTAGTATTA TGTTGGCTGT GGGCTTGTCA TAGGTGGTTT TTATTACTTT	1800
AAGGTATGTC CCTTCTATGC CTGTTTTGCT GAGGGTTTTA ATTCTCGTGC C	1851
(2) INFORMATION FOR SEQ ID NO:293:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 basepairs (A) LENGTH: 668 basepairs (A) (A) LENGTH: 668 basepairs (A)	
(A) LENGTH: 668 base pairs .	
(B) TYPE: nucleic acid () 11	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
grand the Alberta and the second of the seco	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:	
CTTCL COTTC	
CTTGAGCTTC CAAATAYGGA AGACTGGCCC TTACACASGT CAATGTTAAA ATGAATGCAT	60
TTCAGTATTT TGAAGATAAA ATTRGTAGAT CTATACCTTG TTTTTTGATT CGATATCAGC	120
ACCRTATAAG AGCAGTGCTT TGGCCATTAA TTTATCTTTC ATTRTAGACA GCRTAGTGYA	180
GAGTGGTATT TCCATACTCA TCTGGAATAT TTGGATCAGT GCCATGTTCC AGCAACATTA	240
ACGCACATTC ATCTTCCTGG CATTGTACGG CCTGTCAGTA TTAGACCCAA AAACAAATTA	300
CATATCTTAG GAATTCAAAA TAACATTCCA CAGCTTTCAC CAACTAGTTA TATTTAAAGG	360
AGAAAACTCA TTTTTATGCC ATGTATTGAA ATCAAACCCA CCTCATGCTG ATATAGTTGG	420
CTACTGCATA CCTTTATCAG AGCTGTCCTC TTTTTGTTGT CAAGGACATT AAGTTGACAT	480
CGTCTGTCCA GCAGGAGTTT TACTACTTCT GAATTCCCAT TGGCAGAGGC CAGATGTAGA	540
GCAGTCCTAT GAGAGTGAGA AGACTTTTTA GGAAATTGTA GTGCACTAGC TACAGCCATA	600
GCAATGATTC ATGTAACTGC AAACACTGAA TAGCCTGCTA TTACTCTGCC TTCAAAAAAA	660
AAAAAAA	668
(2) INFORMATION FOR SEQ ID NO:294:	
(i)- SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 1512 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294;	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294;	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294; GGGTCGCCCA GGGGGGGCGT GGGCTTTCCT CGGGTGGGTG TGGGTTTTCC CTGGGTGGG	60
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294;	60 120 180

ATCTGTTGGC	TACTACTGGC	TTCTCCTCGC	TGTTAAAAGC	AGATGCTGGT	TGAGGTTGAT	240
TCCATGCCGG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTTGCTTCCC	CTGCTGCAGC	GAGAGCGCCA	AGAGCAACGT	GGGCACTTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	GGGGAGACTA	CGATGACAGT	600
GCCTTCATGG	AGCCCAGGTA	CCACGTCCGT	GGAGAAGATC	TGGACAAGCT	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGG : A	CACTGACGTG	720
AACAAGAAGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	$\texttt{CCTCTGCC.} \lambda \texttt{A}$	TGGGAATTCA	780
GAAGTAGTAA	AACTCSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	${\tt AAGATAAATT}$	AATGGCCAAA	GCACTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGGTATAGAT	CTACTAATTT	TATCTTCAAA	ATACTGAAAT	GCATTCATTT	1080
TAACATTGAC	GTGTGTAAGG	GCCAGTCTTC	CGTATTTGGA	AGCTCAAGCA	TAACTTGAAT	1140
GAAAATATTT	TGAAATGACC	TAATTATCTM	AGACTTTATT	TTAAATATTG	TTATTTTCAA	1200
AGAAGCATTA	GAGGGTACAG	$\mathtt{TTTTTTTTT}$	TTAAATGCAC	TTCTGGTAAA	TACTTTTGTT	1260
GAAAACACTG	AATTTGTAAA	AGGTAATACT	TACTATTTTT	CAATTTTTCC	CTCCTAGGAT	1320
TTTTTTCCCC	TAATGAATGT	AACATGGCAA	AATTTGCCCT	GAAATAGGTT	TTACATGAAA	1380
ACTCCAAGAA	AAGTTAAACA	TGTTTCAGTG	AATAGAGATC	CTGCTCCTTT	GGCAAGTTCC	1440
TAAAAAACAG	TAATAGATAC	GAGGTGATGC	GCCTGTCAGT	GGCAAGGTTT	AAGATATTTC	1500
TGATCTCGTG	CC					1512

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGGTCGCCCA	GGGGGSCCGT	GGGCTTTCCT	CGGGTGGGTG	TGGGTTTTCC	CTGGGTGGGG	60
TGGGCTGGGC	TRGAATCCCC	TGCTGGGGTT	GGCAGGTTTT	GGCTGGGATT	GACTTTTYTC	120
TTCAAACAGA	TTGGAAACCC	GCAGTTACCT	GCTAGTTGGT	GAAACTGGTT	GGTAGACGCG	180
ATCTGTTGGC	TACTACTGGC	TTCTCCTGGC	TGTTAAAAGC	AGATGGTGGT	TGAGGTTGAT	240
TCCATGCCGG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTTGCTTCCC	CTGCTGCAGG	GAGAGCGGCA	AGAGCAACGT'	GGGCACTTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	CGGGAGACTA	CGATGACAGY	600
GCCTTCATGG	AKCCCAGGTA	CCACGTCCFT	GGAGAAGATC	TGGACAAGCT'	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGGGA	CACKGAYGTG	720
AACAAGARGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	CCTCTGCCAA	TGGGAATTCA	780
GAAGTAGTAA	AACTCSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	AAGATAAATT	AATGGCCAAA	GCACTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGCATGGCCT	CACACCACTG	YTACTTGGTR	TACATGAGCA	AAAACAGCAA	1080
GTSGTGAAAT	TTTTAATYAA	GAAAAAGCG	AATTTAAAAT	GCRCTGGATA	GATATGGAAG	1140
RACTGCTCTC	ATACTTGCTG	TATGTTGTGG	ATCAGCAAGT	ATAGTCAGCC	YTCTACTTGA	1200
GCAAAATRTT	GATGTATCTT	CTCAAGATCT	GGAAAGACGG	CCAGAGAGTA	TGCTGTTTCT	1260

AGTCATCATC	ATGTAATTTG	CCAGTTACTT	TCTGACTACA	AAGAAAAACA	GATGTTAAAA	1320
ATCTCTTCTG	AAAACAGCAA	TCCAGAACAA	GACTTAAAGC	TGACATCAGA	GGAAGAGT'CA	1380
CAAAGGCTTA	AAGGAAGTGA	AAACAGCCAG	CCAGAGGCAT	${\tt GGAAACTTTT}$	AAATTTAAAC	1440
TTTTGGTTTA	ATGTTTTTT	TTTTTGCCTT	ATTATATTA	GATAGTCCCA	AATGAAATWA	1500
CCTATGAGAC	TAGGCTTTGA	GAATCAATAG	ATTCTTTTTT	TAAGAATCTT	TTGCCTAGGA	1560
GCGGTGTCTC	ACGCCTGTAA	TTCCAGCACC	TTGAGAGGCT	GAGGTGGGCA	GATCACGAGA	1620
TCAGGAGATC	GAGACCATCC	TGGCTAACAC	GGTGAAACCC	CATCTCTACT	AAAAATACAA	1680
AAACTTAGCT	GGGTGTGGTG	GCGGGTGCCT	GTAGTCCCAG	CTACTCAGGA	RGCTGAGGCA	1740
GGAGAATGGC	ATGAACCCGG	GAGGTGGAGG	TTGCAGTGAG	CCGAGATCCG	CCACTACACT	1800
CCAGCCTGGG	TGACAGAGCA	AGACTCTGTC	TCAAAAAAA	AAAAAAAA	AAA	1853

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 2184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GGCACGAGAA	TTAAAACCCT	CAGCAAAACA	GGCATAGAAG	GGACATACCT	TAAAGTAATA	60
AAAACCACCT	ATGACAAGCC	CACAGCCAAC	ATAATACTAA	ATGGGGAAAA	GTTAGAAGCA	120
TTTCCTCTGA	GAACTGCAAC	AATAAATACA	AGGATGCTCG	ATTTTGTCAA	ATGCCTTTTC	180
TGTGTCTGTT	GAGATGCTTA	TGTGACTTTG	CTTTTAATTC	TGTTTATGTG	ATTATCACAT	240
TTATTGACTT	GCCTGTGTTA	GACCGGAAGA	GCTGGGGTGT	TTCTCAGGAG	CCACCGTGTG	300
CTGCGGCAGC	TTCGGGATAA	CTTGAGGCTG	CATCACTGGG	GAAGAAACAC	AYTCCTGTCC	360
GTGGCGCTGA	TGGCTGAGGA	CAGAGCTTCA	GTGTGGCTTC	TCTGCGACTG	GCTTCTTCGG	420
GGAGTTCTTC	CTTCATAGTT	CATCCATATG	GCTCCAGAGG	TATATAAAA	TATTTTGTTA	480
TGGATGAAGA	GTATTACGTT	GTGCAGATAT	ACTGCAGTGT	CTTCATCTCT	TGATGTGTGA	540
TTGGGTAGGT	TCCACCATGT	TGCCGCAGAT	GACATGATTT	CAGTACCTGT	GTCTGGCTGA	600
AAAGTGTTTG	${\tt TTTGTGAATG}$	${\tt GATATTGTGG}$	TTTCTGGATC	TCATCCTCTG	TGGGTGGACA	650
GCTTTCTCCA	${\tt CCTTGCTGGA}$	AGTGACCTGC	TGTCCAGAAG	TTTGATGGCT	GAGGAGTATA	720
CCATCGTGCA	TGCATCTTTC	ATTTCCTGCA	TTTCTTCCTC	CCTGGATGGA	CAGGGGGAGC	780
GGCAAGAGCA	ACGTGGGCAC	TTCTGGAGAC	CACAACGACT	CCTCTGTGAA	GACGCTTGGG	840
AGCAAGAGGT	GCAAGTGGTG	CTGCCACTGC	TTCCCCTGCT	GCAGGGGAGC	GGCAAGAGCA	900
ACGTGGTCGC	TTGGGGAGAC	TACGATGACA	GCGCCTTCAT	GGATCCCAGG	TACCACGTCC	960
ATGGAGAAGA	TCTGGACAAG	CTCCACAGAG	CTGCCTGGTG	GGGTAAAGTC	CCCAGAAAGG	1020
ATCTCATCGT	CATGCTCAGG	GACACGGATG	TGAAĆAAGAG	GGACAAGCAA	AAGAGGACTG	1080
CTCTACATCT	GGCCTCTGCC	AATGGGAATT	CAGAAGTAGT	AAAACTCGTG	CTGGACAGAC	1140
GATGTCAACT	TAATGTCCTT	GACAACAAAA	AGAGGACAGC	TCTGACAAAG	GCCGTACAAT	1200
GCCAGGAAGA	TGAATGTGCG	TTAATGTTGC	TGGAACATGG	CACTGATCCA	AATATTCCAG	1260
ATGAGTATGG	AAATACCACT	CTACACTATG	CTGTCTACAA	TGAAGATAAA	TTAATGGCCA	1320
AAGCACTGCT	CTTATACGGT	GCTGATATCG	AATCAAAAAA	CAAGCATGGC	CTCACACCAC	1380
TGCTACTTGG	TATACATGAG	CAAAAACAGC	AAGTGGTGAA	ATTTTTÄATC	AAGAAAAAG	1440
CGAATTTAAA	TGCGCTGGAT	AGATATGGAA	GAACTGCTCT	CATACTTGCT	GTATGTTGTG	1500
GATCAGCAAG	TATAGTCAGC	CCTCTACTTG	AGCAAAATGT	TGATGTATCT	TCTCAAGATC	1560
TGGAAAGACG	GCCAGAGAGT	ATGCTGTTTC	TAGTCATCAT	CATGTAATTT	GCCAGTTACT	1620
TTCTGACTAC	AAAGAAAAAC	AGATGTTAAA	AATCTCTTCT	GAAAACAGCA	ATCCAGAACA	1680
AGACTTAAAG	CTGACATCAG	AGGAAGAGTC	ACAAAGGCTT	AAAGGAAGTG	AAAACAGCCA	1740
GCCAGAGGCA	TGGAAACTTT	TAAATTTAAA	CTTTTGGTTT	AATGTTTTTT	TTTTTTGCCT	1800
TAATAATATT	AGATAGTCCC	AAATGAAATW	ACCTATGAGA	CTAGGCTTTG	AGAATCAATA	1860
GATTCTTTTT	TTAAGAATCT	TTTGGCTAGG	AGCGGTGTCT	CACGCCTGTA	ATTCCAGCAC	1920
CTTGAGAGGC	TGAGGTGGGC	AGATCACGAG	ATCAGGAGAT	CGAGACCATC	CTGGCTAACA	1980
CGGTGAAACC	CCATCTCTAC	TAAAAATACA	AAAACTTAGC	TGGGTGTGGT	GGCGGGTGCC	2040

TGTAGTCCCA	GCTACTCAGG	ARGCTGAGGC	AGGAGAATGG	CATGAACCCG	GGAGGTGGAG	2100
GTTGCAGTGA	GCCGAGATCC	GCCACTACAC	TCCAGCCTGG	GTGACAGAGC	AAGACTCTGT	2160
CTCAAAAAAA	AAAAAAAAA	AAAA				2184

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

TGCACGCATC	GGCCAGTGTC	TGTGCCACGT	ACACTGACGC	CCCCTGAGAT	GTGCACGCCG	60
CACGCGCACG	TTGCACGCGC	GGCAGCGGCT	TGGCTGGCTT	GTAACGGCTT	GCACGCGCAC	120
GCCGCCCCCG	CATAACCGTC	AGACTGGCCT	GTAACGGCTT	GCAGGCGCAC	GCCGCACGCG	180
CGTAACGGCT	TGGCTGCCCT	GTAACCGCTT	GCACGTGCAT	GCTGCACGCG	CGTTAACGGC	240
TTGGCTGGCA	TGTAGCCGCT	TGGCTTGGCT	TTGCATTYTT	TGCTKGGCTK	GGCGTTGKTY	300
TCTTGGATTG	ACGCTTCCTC	CTTGGATKGA	CGTTTCCTCC	TTGGATKGAC	GTTTCYTYTY	360
TCGCGTTCCT	TTGCTGGACT	TGACCTTTTY	TCTGCTGGGT	TTGGCATTCC	TTTGGGGTGG	420
GCTGGGTGTT	TTCTCCGGGG	GGGKTKGCCC	TTCCTGGGGT	GGGCGTGGGK	CGCCCCAGG	480
GGGCGTGGGC	TTTCCCCGGG	TGGGTGTGGG	TTTTCCTGGG	GTGGGGTGGG	CTGTGCTGGG	540
ATCCCCCTGC	TGGGGTTGGC	AGGGATTGAC	TTTTTTCTTC	AAACAGATTG	GAAACCCGGA	600
GTAACNTGCT	AGTTGGTGAA	ACTGGTTGGT	AGACGCGATC	TGCTGGTACT	ACTGTTTCTC	650
CTGGCTGTTA	AAAGCAGATG	GTGGCTGAGG	TTGATTCAAT	GCCGGCTGCT	TCTTCTGTGA	720
AGAAGCCATT	TGGTCTCAGG	AGCAAGATGG	GCAAGTGGTG	CGCCACTGCT	TCCCCTGCTG	780
CAGGGGGAGC	GCCAAGAGCA	ACGTGGGCAC	TTCTGGAGAC	CACAACGACT	CCTCTGTGAA	840
GACGCTTGGG	AGCAAGAGGT	GCAAGTGGTG	CTGCCCACTG	CTTCCCCTGC	TGCAGGGGAG	900
CGGCAAGAGC	AACGTGGKCG	CTTGGGGAGA	CTACGATGAC	AGCGCCTTCA	TGGAKCCCAG	960
GTACCACGTC	CRTGGAGAAG	ATCTGGACAA	GCTCCACAGA	GCTGCCTGGT	GGGGTAAAGT	1020
CCCCAGAAAG	GATCTCATCG	TCATGCTCAG	GGACACTGAY	GTGAACAAGA	RGGACAAGCA	1080
AAAGAGGACT	GCTCTACATC	TGGCCTCTGC	CAATGGGAAT	TCAGAAGTAG	TAAAACTCGT	1140
GCTGGACAGA	CGATGTCAAC	TTAATGTCCT	TGACAACAAA	AAGAGGACAG	CTCTGACAAA	1200
GGCCGTACAA	TGCCAGGAAG	ATGAATGTGC	GTTAATGTTG	CTGGAACATG	GCACTGATCC	1260
AAATATTCCA	GATGAGTATG	GAAATACCAC	TCTACACTAT	GCTGTCTACA	ATGAAGATAA	1320
ATTAATGGCC	AAAGCACTGC	TCTTATACGG	TGCTGATATC	GAATCAAAAA	ACAAGGTATA	1380
GATCTACTAA	TTTTATCTTC	AAAATACTGA	AATGCATTCA	TTTTAACATT	GACGTGTGTA	1440
AGGGCCAGTC	TTCCGTATTT	GGAAGCTCAA	GCATAACTTG	AATGAAAATA	TTTTGAAATG	1500
ACCTAATTAT	CTAAGACTTT	ATTTTAAATA	TTGTTATTTT	CAAAGAAGCA	TTAGAGGGTA	1560
CAGTTTTTTT	TTTTTAAATG	CACTTCTGGT	AAATACTTTT	GTTGAAAACA	CTGAATTTGT	1620
AAAAGGTAAT	ACTTACTATT	TTTCAATTTT	TCCCTCCTAG	GATTTTTTC	CCCTAATGAA	1680
TGTAAGATGG	CAAAATTTGC	CCTGAAATAG	GTTTTACATG	AAAACTCCAA	GAAAAGTTAA	1740
ACATGTTTCA	GTGAATAGAG	ATCCTGCTCC	TTTGGCAAGT	ТССТАААААА	CAGTAATAGA	1800
TACGAGGTGA	TGCGCCTGTC	AGTĠGCAAGG	TTTAAGATAT	TTCTGATCTC	GTGCC	1855

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CLAIMS

- 1. An isolated DNA molecule, comprising:
- (a) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297;
- (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or
- (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.
- 2. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by a nucleotide sequence that:
- (a) hybridizes to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and
- (b) is at least 80% identical to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

- 3. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by:
- (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or
- (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained.
- 4. An isolated DNA or RNA molecule comprising a nucleotide sequence complementary to a DNA molecule according to any one of claims 1-3.
- 5. A recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.
- 6. A host cell transformed or transfected with an expression vector according to claim 5.
- 7. A polypeptide comprising an amino acid sequence encoded by a DNA molecule according to any one of claims 1-3.
- 8. A polypeptide according to claim 7 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.
- 9. A monoclonal antibody that binds to a polypeptide according to claim 7.

- 10. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.
- A method for determining the presence of breast cancer in a patient comprising detecting within a biological sample, at least one polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.
- 12. The method of claims 10 or 11 wherein the biological sample is a portion of a breast tumor.
- 13. The method of claim 10 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody according to claim 9.
- 14. The method of claim 11 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.
- 15. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, an RNA molecule encoding at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

- 16. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.
- 17. The method of claims 15 or 16 wherein the biological sample is a portion of a breast tumor.
 - 18. The method of claim 15 wherein the step of detecting comprises:
- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.
 - 19. The method of claim 16 wherein the step of detecting comprises:
- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

- 20. A method for monitoring the progression of breast cancer in a patient, comprising:
- (a) detecting an amount, in a biological sample, of at least one polypeptide according to claim 7 at a first point in time;
 - (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.
- A method for monitoring the progression of breast cancer in a patient, comprising:
- detecting in a biological sample an amount of at least one polypeptide at a first point in time, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;
 - (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.
- 22. The method of claims 20 or 21 wherein the biological sample is a portion of a breast tumor.
- 23. The method of claim 20 wherein the step of detecting comprises contacting a portion of the biological sample with a monoclonal antibody according to claim 9.
- 24. The method of claim 21 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252,

256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

- 25. The method of claim 20 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.
- 26. A method for monitoring the progression of breast cancer in a patient, comprising:
- (a) detecting an amount, within a biological sample, of at least one RNA molecule encoding a polypeptide according to claim 7 at a first point in time;
 - (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.
 - 27. The method of claim 26 wherein the step of detecting comprises:
- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7.
- 28. A method for monitoring the progression of breast cancer in a patient, comprising:
- (a) detecting an amount, within a biological sample, of at least one RNA molecule at a first point in time, the RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 4167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

- 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;
 - (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.
- 29. A pharmaceutical composition, comprising a polypeptide according to claim 7 and a physiologically acceptable carrier.
- A pharmaceutical composition for inhibiting the development of breast cancer, comprising a polypeptide and a physiologically acceptable carrier, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.
- 31. A vaccine, comprising a polypeptide according to claim 7 and an immune response enhancer.

Agricultural Company

- 32. A vaccine, comprising a DNA molecule according to any one of claims 1-3.
- 33. A vaccine, comprising a recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.
- 34. A vaccine for inhibiting the development of breast cancer, comprising a polypeptide and an immune response enhancer, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

- 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.
- 35. A pharmaceutical composition according to either of claims 29 or 30, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient, comprising administering to a patient.
- 36. A vaccine according to any one of claims 31-34, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient.
 - 37. A diagnostic kit comprising:
 - (a) one or more monoclonal antibodies according to claim 9; and
 - (b) a detection reagent.
 - 38. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290; and
 - (b) a detection reagent.
- 39. The kit of any one of claims 37 or 38 wherein the monoclonal antibody(s) are immobilized on a solid support.
- 40. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule according to claim 4.
- 41. The kit of claim 40, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule according to claim 4.

- 42. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.
- 43. The kit of claim 42, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.
- 44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe containing at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

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- 45. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe comprising at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.
- 46. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA molecule according to claim 4.
- 47. The kit of claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.
- 48. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145,

153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

49. The kit of claim 48, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

1722

CONA PREPARED FROM NORMAL BREAST TISSUE FROM THE SAME PATIENT

DNA PREPARED FROM BREAST TUMOR

■ B13Ag1

Fig. 1

SUBSTITUTE SHEET (RULE 26)

SPEAST TUMOR TRYA.

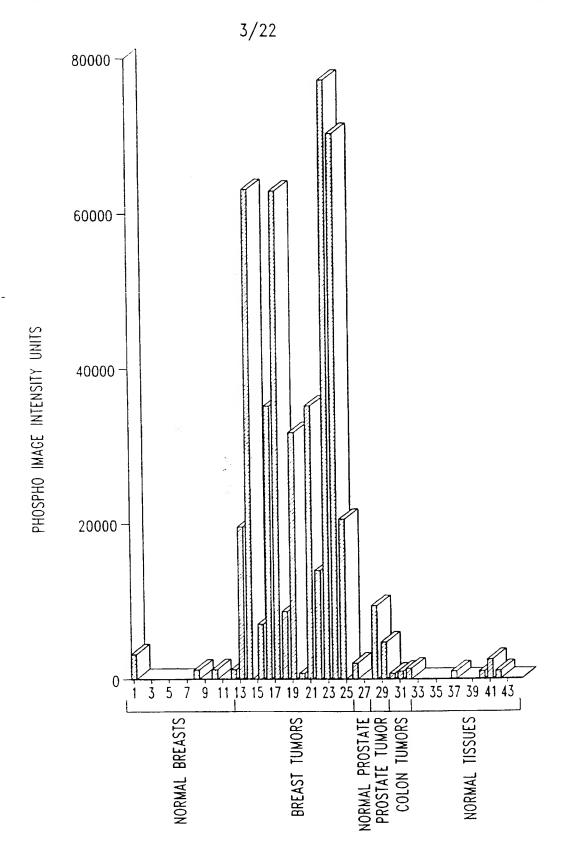


Fig. 3.

SUBSTITUTE SHEET (RULE 26)

GENOMIC CLONE MAP

Xbal

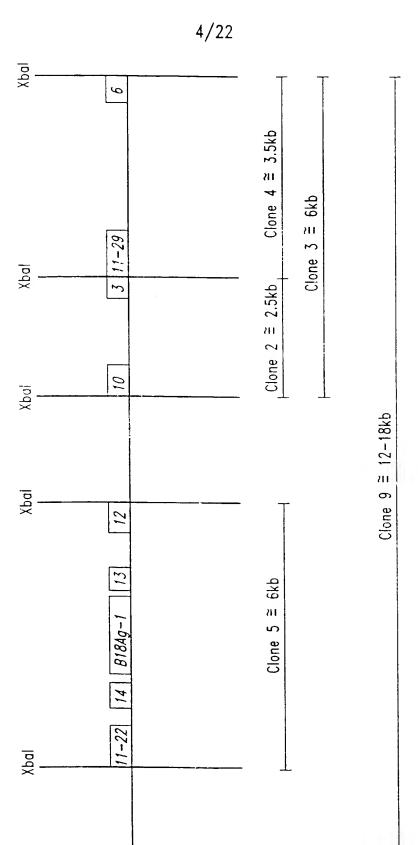
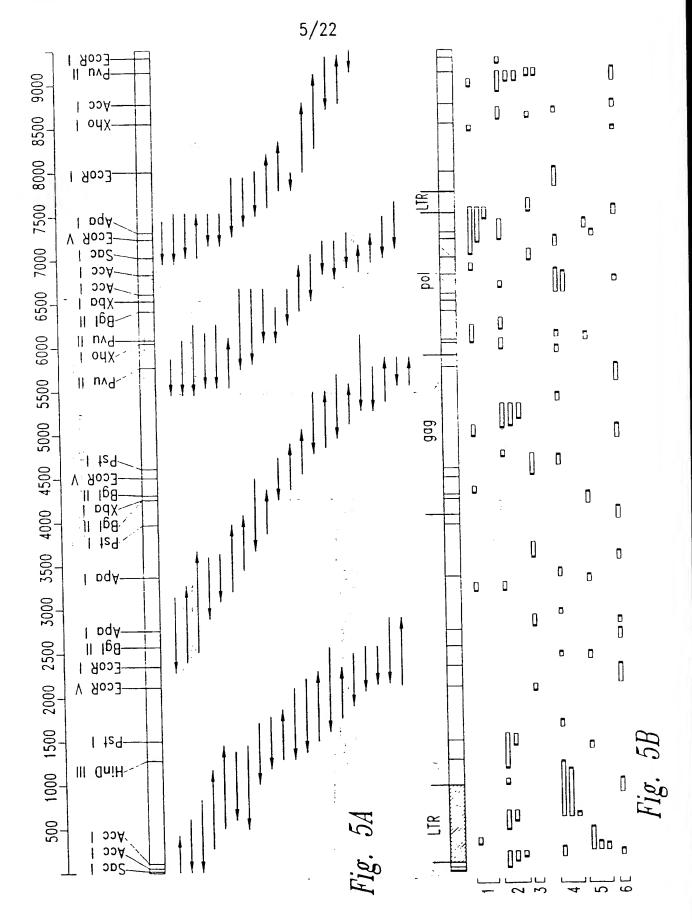


FIG. 4



SUBSTITUTE SHEET (RULE 26)

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B18Ag1

		Leu 5							48
		GAC Asp							96
		AAA Lys							144
		GAG Glu							192
		TAC Tyr							240
		TTG Leu 85							288
		AAA Lys						TCA Ser	336
_		AGC Ser							363

NUCLEOTIDE SEQUENE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC	TGGGCACAGT	GGETCATACC	TGTAATCCTG	ACCGTTTCAG	AGGCTCAGGT	60
CG	CTTGAGCCCA	AGATTTCAAG	ACTAGTCTGG	GTAACATAGT	GAGACCCTAT	120
- AA	AAATAAAAA	ATGAGCCTGG	TGTAGTGGCA	CACACCAGCT	GAGGAGGGAG	180
CT	'AGGAGA				•	196

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC	TTGGGGGCTC	TGACTAGAAA	TTCAAGGAAC	CTGGGATTCA	AGTCCAACTG	60
AC	TTACACTGTG	GNCTCCAATA	AACTGCTTCT	TTCCTATTCC	CTCTCTATTA	120
AA	GGAAAACGAT	GTCTGTGTAT	AGCCAAGTCA	GNTATCCTAA	AAGGAGATAC	180
ΑТ	TAAATATCAG	AATGTAAAAC	CTGGGAACCA	GGTTCCCAGC	CTGGGATTAA	240
СА	AGAAGACTGA	ACAGTACTAC	TGTGAAAAGC	CCGAAGNGGC	AATATGTTCA	300
TT	GAAGGATGGC	TGGGAGAATG	AATGCTCTGT	CCCCCAGTCC	CAAGCTCACT	360
СТ	CCTTTATAGE	CTAGGAGA				388

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC	CTATAATCAT	GTTTCTCATT	ATTTTCACAT	TTTATTAACC	AATTTCTGTT	60
AA	AATATGAGGG	AAATATATGA	AACAGGGAGG	CAATGTTCAG	ATAATTGATC	120
TG	ATTTCTACAT	CAGATGCTCT	TTECTTTCCT	GTT-TATT-TEC	TTTTTATTTC	180
GG	TCGAATGTAA	TAGCTTTGTT	TCAAGAGAGA	GTTTTGGCAG	TTTCTGTAGC	240
				TAGGAGGTGT	CGTGGGAGAC	300
СΤ	ATTTTTTCCA	TATTTGGGCA	ACTACTA	,: " · · · · · · · · · · · · · · · · · ·		337

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B13Ag1b

60	GCATAAACTG	CACCTGAACG	ATTTAACCCC	CTTTCCATTT	CATACAGTGC	GC
120	CATTTAAACC	CTTTGCTCTT	AATAAGGAGA	TACTGTAAAC	TGGTGTTTTT	GC
180	ACACTCCTTA	GTTCCTTTTT	GTTTTTACCG	ACGCTCGAGG	TICATATTIT	AT
240	TTTTAACATT	TCCTGGCAGC	ATTTTTCTT	GGAACAAGAT	TAAGTCGITI	TT
300	AAATCAAGGC	TCACAGTTGC	TCACTGTTTC	GGACTGCTGG	TGTGTCTG66	TT
360	GATAAACGGT	AACTGGACCG	TTTTATTTGA	AATTTTTTIG	AAGAAAAAA	CC
420	AAGTTGCACT	GCACCTCCTT	ATGGTTTATT	ATAGTTTTAA	GCTGCTGTAT	CG
480	GGACTTTTNT	ANAGTCACAG	NTTTANTCAC	NATAGAAAGT	GGGGNTTTTG	GG
540	AGGCTCACAG	CGGCAGATGA	TTTCGGGTGG	AAGGGCTGNT	CTGAGCTAAA	NA
571			А	GGGAACTNCT	TCTTAGAGGG	TC

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B13Ag1a

Α	ATAACTTAAA	TATATTTTGA	TCACCCACTG	GGGTGATAAG	ACAATAGATA	60
Τ	TCCAAAAAGC	ATAAAACCAA	AGTATCATAC	CAAACCAAAT	TCATACTGCT	120
CC	GCACTGAAAC	TTCACCTTCT	AACTGTCTAC	CTAACCAAAT	TCTACCCTTC	180
- 5G	TGCGTGCTCA	CTACTCTTTT	TTTTTTTT	TATNTTTTGG	AGATGGAGTC	240
ĴΑ.	GCCCAGGGGT	GGAGTACAAT	GGCACAACCT	CAGCTCACTG	NAACCTCCGC	300
Т	CATGAGATTC	TCCTGNTTCA	IGCOTTECCAG	TAGCTGGGAC	TACAGGTGTG	360
TG	CCTGGNTAAT	CTTTTTTNGT	TTTNGGGTAG	AGATGGGGGT	TTTACATGTT	420
TG	GINTCGAACT	CCTGACCTCA	AGTGATCCAC.	CCACCTCAGG	CTCCCAAAGT	480
TΑ	CAGACATGAG	CCACTGNGCC	CAGNCCTGGT	GCATGCTCAC	TTCTCTAGGC	540
						549

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG	CACATGCAGA	ATATTCTATC	GGTACTTCAG	CTATTACTCA	TTTTGATGGC	60
AG	CCTATCCTCA	AGATGAGTAT	TTAGAAAGAA	TTGATTTAGC	GATAGACCAA	120
GC	ACTCTGACTA	CACGAAATTG	TTCAGATGTG	ATGGATTTAT	GACAGTTGAT	180
GA	GATTATTAAG	TGATTATTTT	AAAGGGAATC	CATTAATTCC	AGAATATCTT	240
TC	AAGATGATAT	AGAAATAGAA	CAGAAAGAGA	CTACAAATGA	AGATGTATCA	300
TA	TTGAAGAGCC	TATAGTAGAA	AATGAATTAG	CTGCATTTAT	TAGCCTTACA	360
TT	TTCCTGATGA	ATCTTATATT	CAGCCATCGA	CATAGCATTA	CCTGATGGGC	420
GA	ATAATAGAAA	CTGGGTGCGG	GGCTATTGAT	GAATTCATCC	NCAGTAAATT	480
AC	AAAATATAAC	TCGATTGCAT	TTGGATGATG	GAATACTAAA	TCTGGCAAAA	540
GG	AGCTACTAGT	AACCTCTCTT	TTTGAGATGC	AAAATTTTCT	TTTAGGGTTT	600
СТ	ACTTTACGGA	TATTGGAGCA	TAACGGGA			638

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B3CA3c

ACTGATGGAT	GTCGCCGGAG	GCGAGGGGCC	TTATCTGATG	CTCGGCTGCC	TGTTCGTGAT	60
GTGCGCGGCG	ATTGGGCTGT	TTATCTCAAA	CACCGCCACG	GCGGTGCTGA	TGGCGCCTAT	120
TGCCTTAGCG	GCGGCGAAGT	CAATGGGCGT	CTCACCCTAT	CCTTTTGCCA	TGGTGGTGGC	180
GATGGCGGCT	TCGGCGGCGT	TTATGACCCC	GGTCTCCTCG	CCGGTTAACA	CCCTGGTGCT	240
TGGCCCTGGC	AAGTACTCAT	TTAGCGATTT	TGTCAAAATA	GGCGTG A		286

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B9CG1

AG	CAGCCCCTTC	TTCTCAATTT	CATCTGTCAC	TACCCTGGTG	TAGTATCTCA	60
CA	TTTTTATAGC	стсстссстб	GTCTGTCTTT	TGATTTTCCT	GCCTGTAATC	120
AC	ATAACTGCAA	GTAAACATTT	CTAAAGTGTG	GTTATGCTCA	TGTCACTCCT	180
AA	ATAGTTTCCA	TTACCGTCTT	AATAAAATTC	GGATTTGTTC	TTTNCTATTN	240
$C \Lambda$	CCTATGACCG	^^				268

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B9CG3

60	AACCAAGGCC	TAAACTCCTA	CTCTACTGTG	GGTTTGAGCT	CAAAGCCAGT	4G
120	AATTTCCTAT	TACCCATGCA	TATAAACATG	GGATTTTTAT	AATGGTGGCA	TΑ
180	TAAAAGCCTA	AATCTATTTT	CAATAAAAAT	TACATTTAAA	TATATTCTTC	GA
240	CACCAGTCAA	AGGTATAAAT	AGAGGGTATA	GTGTTTAATG	TTAGGTAAGA	AG
261		•		Α	CCTATGACCG	TG

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B2CA2

TTGATTCGT	61
TTTTNTGTT	120
GTCTTCTGC	180
	20

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B3CA1

GG	GCATGGACGC	AGACGCCTGA	CGTTTGGCTG	AAAATCTTTC	ATTGATTCGT	60
ΑT	AGGAAAATTC	CCAAAGAGGG	AATGTCCTGT	TGCTCGCCAG	TTTTTNTGTT	120
GG	ANAAGGCAAN	GAGCTCTTCA	GACTATTGGN	ÁTTNTCGTTC	GGTCTTCTGC	180
CG	NCTTGCNANG	ATCTTCAT		ı		208

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B3CA2

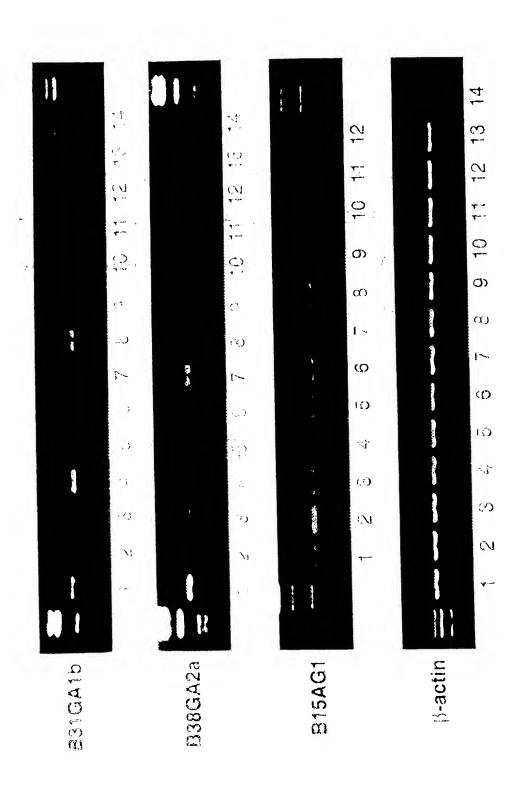
GG	GCATGGACGC	AGACGCCTGA	CGTTTGGCTG	AAAATCTTTC	ATTGATTCGT	60
ΑT	AGGAAAATTC	CCAAAGAGGG	AATGTCCTGT	TGCTCGCCAG	TTTTTNTGTT	120
GG	ANAAGGCAAN	GAGCTCTTCA	GACTATTGGN	ATTNTCGTTC	GGTCTTCTGC	180
CG	NCTTGCNANG	ATCTTCAT				208

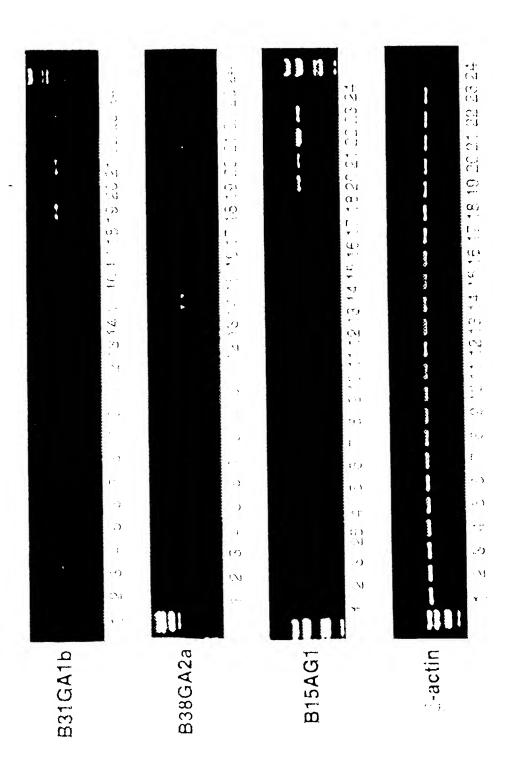
NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B3CA3

ΑG	GGAGCAAGGA	GAAGGCATGG	AGAGGCTCAN	GCTGGTCCTG	GCCTACGACT	60
СТ	GTCGCCGGGG	ATGGTGGAGA	ACTGAAGCGG	GACCTCCTCG	AGGTCCTCCG	120
TC	NCCGTCCAGG	AGGAGGGTCT	·TTCCGTGGTC	TNGGAGGAGE	GGGGGGAGAA	180
TC	ATGGTCNACA	TCCC		4 1 8 °		204

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE BREAST-TUMOR SPECIFIC cDNA B4CA1

C	AGGAGCGGGT	AGAGTGGCAC	CATTGAGGGG	ATATTCAAAA	ATATTATTT	60
ſĞ	ATAGTTGCTG	AGTTTTTCTT	TGACCCATGA	GTTATATTGG	AGTTTATTTT	120
CC	AATCGCATGG	ACATGTTAGA	CTTAITTITCT	GTTAATGATT	NCTATTTTTA	180
āΑ	TTTGAGAAAT	TGGTTNTTAT	TATATCAATT	TTTGGTATTT	GTTGAGTTTG	240
GC	TTAGTATGTG	ACCA				264





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	997 (09.04.97) nber 1997 (11.12.9		(AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European pate (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, I'LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, C
1124 Columbia Street, Seattle,		 2 0	
(72) Inventors: FRUDAKIS, Tony, N WA 99232-0232 (US). SMIT Place Southeast, Everett, WA 9 G.; 2843 - 122nd Place N.E., E	TH, John, M.; 208 98208 (US). REEL	3 – 116 D, Steve	h With international search report.
(74) Agents: MAKI, David, J. et a 6300 Columbia Center, 701 I 98104-7092 (US).	al.; Seed and Be Fifth Avenue, Sea	rry LL attle, W	P.
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(54) Title: COMPOSITIONS AND M	ETHODS FOR TH	IE TRE	ATMENT AND DIAGNOSIS OF BREAST CANCER
(57) Abstract	* * * *	•	
sequences that are preferentially express	sed in breast tumor orising such compo eptides may also	tissue, ounds a	breast cancer are disclosed. The compounds provided include nucleot as well as polypeptides encoded by such nucleotide sequences. Vacci e also provided and may be used, for example, for the prevention for the production of antibodies, which are useful for diagnosing
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Application No Internatio PCT/U₂ 98/06939

a. classification of subject matter IPC 6 CO7K14/47 CO7I CO7K14/15 C12Q1/68 G01N33/574 C07K14/82 A61K38/17 A61K39/00 According to International Patent Classification (IPC) or to both national classification and IPC **B. FIELDS SEARCHED** Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) C. DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No. Υ 1,2, WERNER T ET AL: "S71 IS A PHYLOGENETICALLY DISTINCT HUMAN ENDOGENOUS 4-10,12,RETROVIRAL ELEMENT WITH STRUCTURAL AND 13,15, SEQUENCE HOMOLOGY TO SIMIAN SARCOMA VIRUS 17,18, (SSV)" 20,22, 23, VIROLOGY, vol. 174, no. 1, January 1990, 25-27, pages 225-238, XP000670325 29, 31-33, 35 - 37, 39-41, 44,46,47 see the whole document Further documents are fisted in the continuation of box C. Patent family members are listed in annex. Х Special categories of cited documents: "T" later document published after the international filing date or priority date and not in conflict with the application but "A" document defining the general state of the art which is not cited to understand the principle or theory underlying the considered to be of particular relevance invention "E" earlier document but published on or after the international "X" document of particular relevance; the claimed invention filing date cannot be considered novel or cannot be considered to *L* document which may throw doubts on priority claim(s) or which is cried to establish the publication date of another involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention citation or other special reason (as specified) cannot be considered to involve an inventive step when the document is combined with one or more other such docu-"O" document referring to an oral disclosure, use, exhibition or ments, such combination being obvious to a person skilled *P* document published prior to the international filing date but in the art. later than the priority date claimed "&" document member of the same patent family Date of the actual completion of the international search Date of mailing of the international search report 26 January 1999 31 August 1998 Name and mailing address of the ISA **Authorized officer** European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijewijk Tel. (+31-70) 340-2040, Tx. 31 651 epo ni, Fax: (+31-70) 340-3016

Hagenmaier, S

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International Application No PCT/US 98/06939

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PCT/US 98/06939

	tion) DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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		20,22, 23, 25-27,
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		4-10,12, 13,15, 17,18, 20,22, 23,
		25-27, 29, 31-33, 35-37, 39-41,
	see the whole document	44,46,47

Intel onal application No.

PCT/US 98/06939

Box I	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This Inte	ernational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1.	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2.	Claims Nos.: because they relate to parts of the international Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically:
3	Claims Nos
لــا ٠٠	because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
··	
Box II	Observations where unity of invention is lacking (Continuation of Item 2 of Itrst sheet)
This Inte	emational Searching Authority found multiple inventions in this international application, as follows:
	FIRTHER THEORY I I I
se	e FURTHER INFORMATION sheet
1.	As all required additional search fees were timely paid by the applicant, this International Search Report covers all
L	searchable claims.
2.	As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
	As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.	As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. X	No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
	see FURHTER INFORMATION sheet, subject 1.
	See Founting Information Sheet, Subject 1.
Remar	k on Protest The additional search-fees were accompanied by the applicant's protest.
	No protest accompanied the payment of additional search fees.
	

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1992)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33, 35-37,39-41,44,46,47 (all partially)

Invention 1:
Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 1, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to seq. ID 1, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 1, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

2. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33, 35-37,39-41,44,46,47 (all partially)

Invention 2-75:
Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 3, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 3, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 3, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences 4-26, 28-77

3. Claims: 3 (completely), 4-10,12,13,15,17,18,20,22,23,25-27, 29,31-33,35-37,39-41,44,46,47 (all partially)

Invention 76:
Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 141, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 141, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 141, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

4. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33, 35-37,39-41,44,46,47 (all partially)

Invention 77-200:
Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 142, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 142, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 142, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences 143,146-152,154-166,168-176,178-192,194-198,200-204,206,207,2 09-214,216,218,219,221-240,243-245,247,250,251,253,255,257-26 6,268,269,271-273,275,276,278,280,281,284,288 and 291-297

5. Claims: 11,12,14,16,17,19,21,22,24,30,34,35,36,38,39,42,43, 45,48,49 (all partially)

Invention 201-241:
Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 78, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 78, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 78, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences
78-86,144,145,153,167,177,193,199,205,208,215,217,220,241,242,246,248,249,252,256,267,270,274,277,279,282,283,285-287,289,

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